

97975

From: Chan, Christina  
Sent: Wednesday, July 02, 2003 1:30 PM  
To: Mertz, Prema; STIC-Biotech/ChemLib  
Subject: RE: 09/521,195

**Please rush. Thanks Chris**

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: **Mertz, Prema**  
Sent: Wednesday, July 02, 2003 1:02 PM  
To: Chan, Christina  
Subject: 09/521,195

Please conduct an interference search on SEQ ID NO:1-2.

Thanks  
--Prema Mertz--  
Prema Mertz, Ph.D.  
Primary Examiner  
Art Unit 1646  
Mailbox 10D-19  
Crystal Mall 1, Room 10E-01  
United States Patent & Trademark Office  
# (703) 308-4229

Christina-

Please RUSH this search on an after-final for me.

Thanks.

--Prema--

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_



Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of results. These databases were split into two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions, **.rnpn** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions, **.rapn** and **.rapn**

*The Pending database search results should not be left in the case because they contain data that is confidential.*



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2003, 12:30:34 ; Search time 149 Seconds  
(without alignments)  
2384.214 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845  
Sequence: 1 MRDYDEVIAFLGEMGFQRL.....KTRDSMTEENPKVITAF 551

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents\_AA\_Main:\*

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26: /cgn2\_6/ptodata/1/paa/US102.COMB.pep.\*  
27: /cgn2\_6/ptodata/1/paa/US60.COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 1          | 2845  | 100.0       | 551    | 1  | PCT-US02-17456-38 |
| 2          | 2845  | 100.0       | 551    | 19 | US-09-521-195B-1  |
| 3          | 2845  | 100.0       | 551    | 19 | US-09-521-195B-1  |
| 4          | 2845  | 100.0       | 551    | 19 | US-09-521-195B-1  |
| 5          | 2845  | 100.0       | 551    | 19 | US-09-521-195B-1  |
| 6          | 2845  | 100.0       | 551    | 19 | US-09-521-195B-1  |

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|----|--------|------|-----|----|----------------------|-------------------|
| 7  | 2470   | 86.8 | 553 | 19 | US-09-521-195B-22    | Sequence 22, Appl |
| 8  | 2454.5 | 86.3 | 616 | 27 | US-60-230-445-1548   | Sequence 1548, Ap |
| 9  | 2247   | 79.0 | 527 | 27 | US-60-230-445-1385   | Sequence 1385, Ap |
| 10 | 2218   | 78.0 | 537 | 1  | PCT-US01-08631-33308 | Sequence 33388, A |
| 11 | 2218   | 78.0 | 557 | 1  | PCT-US02-17382-202   | Sequence 202, App |
| 12 | 2218   | 78.0 | 557 | 1  | PCT-US02-17456-39    | Sequence 39, Appl |
| 13 | 2218   | 78.0 | 557 | 1  | PCT-US02-17456-40    | Sequence 40, Appl |
| 14 | 2218   | 78.0 | 557 | 19 | US-09-521-195B-3     | Sequence 3, Appl1 |
| 15 | 2218   | 78.0 | 557 | 19 | US-09-521-195B-3     | Sequence 3, Appl1 |
| 16 | 2218   | 78.0 | 557 | 21 | US-09-798-743A-1     | Sequence 1, Appl1 |
| 17 | 2218   | 78.0 | 557 | 21 | US-09-798-743A-1     | Sequence 27, Appl |
| 18 | 2164   | 76.1 | 557 | 19 | US-09-521-195B-27    | Sequence 27, Appl |
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| 20 | 2164   | 76.1 | 557 | 21 | US-09-798-743A-3     | Sequence 3, Appl1 |
| 21 | 2164   | 76.1 | 557 | 21 | US-09-798-743A-3     | Sequence 297, App |
| 22 | 1955   | 68.7 | 400 | 27 | US-60-258-275-297    | Sequence 296, App |
| 23 | 1582   | 55.6 | 498 | 27 | US-60-230-445-1504   | Sequence 1504, Ap |
| 24 | 1557   | 54.7 | 410 | 27 | US-09-614-150-13629  | Sequence 13629, A |
| 25 | 857    | 30.1 | 548 | 20 | US-60-167-245-517    | Sequence 517, App |
| 26 | 857    | 30.1 | 548 | 27 | US-60-167-245-517    | Sequence 276, App |
| 27 | 857    | 30.1 | 548 | 27 | US-60-191-637-13670  | Sequence 13670, A |
| 28 | 857    | 30.1 | 548 | 27 | US-60-219-005-153    | Sequence 153, App |
| 29 | 857    | 30.1 | 548 | 27 | US-09-791-537-21414  | Sequence 21414, A |
| 30 | 852    | 29.9 | 548 | 21 | US-60-173-464-24599  | Sequence 24599, A |
| 31 | 821    | 28.9 | 567 | 27 | US-60-191-637-9311   | Sequence 9311, Ap |
| 32 | 819    | 28.8 | 567 | 20 | US-09-614-150-31854  | Sequence 31854, A |
| 33 | 819    | 28.8 | 567 | 27 | US-60-191-637-31426  | Sequence 31426, A |
| 34 | 819    | 28.8 | 567 | 27 | US-60-191-637-31426  | Sequence 24934, A |
| 35 | 801    | 28.2 | 518 | 27 | US-60-145-989-331    | Sequence 331, App |
| 36 | 797.5  | 28.0 | 577 | 1  | PCT-US01-04098A-1029 | Sequence 1029, Ap |
| 37 | 773.5  | 27.2 | 561 | 20 | US-09-614-150-9282   | Sequence 9282, Ap |
| 38 | 773.5  | 27.2 | 561 | 27 | US-60-167-217-9334   | Sequence 9334, Ap |
| 39 | 773.5  | 27.2 | 561 | 27 | US-60-191-637-9311   | Sequence 9311, Ap |
| 40 | 748.5  | 26.3 | 585 | 1  | PCT-US01-04098A-2997 | Sequence 2997, Ap |
| 41 | 704    | 24.7 | 555 | 25 | US-10-177-488-105    | Sequence 105, App |
| 42 | 703    | 24.7 | 555 | 1  | PCT-US01-04098A-1913 | Sequence 1913, Ap |
| 43 | 703    | 24.7 | 555 | 1  | PCT-US02-17456-34    | Sequence 34, Appl |
| 44 | 703    | 24.7 | 555 | 1  | PCT-US02-17456-35    | Sequence 35, Appl |
| 45 | 703    | 24.7 | 555 | 25 | US-10-177-488-104    | Sequence 104, App |

#### ALIGNMENTS

RESULT 1  
PCT-US02-17456-38  
Sequence 38, Application PC/TUS0217456  
GENERAL INFORMATION:  
APPLICANT: EXELIXIS, INC.  
FILE REFERENCE: EX02-086C-PC  
CURRENT APPLICATION NUMBER: PCT/US02/17456  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 60/296,076  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/328,605  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/357,253  
PRIOR FILING DATE: 2002-02-15  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 38  
LENGTH: 551  
TYPE: PRT  
ORGANISM: Homo sapiens  
PCT-US02-17456-38

Query Match 100.0%; Score 2845; DB 1; Length 551;  
Best Local Similarity 100.0%; Pred. No. 2.3e-257;  
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 AMRNSVPLRLRGREVPHSCSRYLATIANFSALGLEPGRVDJGQLEQESCLDGMERS 120
Qy 121 QDYVLSVTVTEMLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLEFATMAVQ 180
Db 121 QDYVLSVTVTEMLVCEDMNKVPLTSLFFVGVLLGSFVSGQLSDRFGRKNVLEFATMAVQ 180
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Db 181 TGFSFQIPISSIMEMFTVLFVYGMQGISNYVAFLIGTEILGKSVRIIFSTLGCTFEA 240
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Db 241 VGYMLPLFAFIRDMRMMLLATVPGVLCVPLMFIPESPRMILISQRRFREAEIIOKA 300
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Db 301 AKMNNTPAVPVIDSVSEELNPLKQKAFILDFRTRNIAIMTMSLLMLTSVGFALS 360
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Db 481 LGAVNRMPLPYIVGSLTVLIGITLFFPSLGMTLPETLEQMKVKWFRSGKTRDSMET 540
Qy 541 EENPKVLTIAF 551
Db 541 EENPKVLTIAF 551

RESULT 2
US-09-521-195-1
; Sequence 1, Application US/09521195
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: TRANSPORTER GENES
; FILE REFERENCE: 06501-057001
; CURRENT APPLICATION NUMBER: US/09/521,195
; CURRENT FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: JP 10/156660
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 9/260972
; PRIOR FILING DATE: 1997-09-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04009
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 1
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-521-195-1

Query Match 100.0%; Score 2845; DB 19; Length 551;
Best Local Similarity 100.0%; Pred. No. 2,3e-257;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 421 DYFFLSIGVLMGKFGITSAFSLMYETAELVPTLVRNAVGVSTASRGVSIAPFVY 480
Db 421 DYFFLSIGVLMGKFGITSAFSLMYETAELVPTLVRNAVGVSTASRGVSIAPFVY 480
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Db 481 LGAVNRMPLPYIVGSLTVLIGITLFFPSLGMTLPETLEQMKVKWFRSGKTRDSMET 540
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Db 541 EENPKVLTIAF 551

RESULT 3
US-09-521-195b-1
; Sequence 1, Application US/09521195b
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: TRANSPORTER GENES
; FILE REFERENCE: 06501-057001
; CURRENT APPLICATION NUMBER: US/09/521,195b
; CURRENT FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: JP 10/156660
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 9/260972
; PRIOR FILING DATE: 1997-09-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04009
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 1
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-521-195b-1

Query Match 100.0%; Score 2845; DB 19; Length 551;
Best Local Similarity 100.0%; Pred. No. 2,3e-257;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4  
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; Sequence 37, Application PC/TUS0217456  
; GENERAL INFORMATION:  
; APPLICANT: EXELTIS, INC.  
; TITLE OF INVENTION: SLIC22AS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-086C-PC  
; CURRENT APPLICATION NUMBER: PCT/US02/17456  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 551  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-17456-37

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Best Local Similarity 99.6%; Pred. No. 3.1e-256;  
Matches 549; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 5  
US-60-230-445-1642  
; Sequence 1642, Application US/60230445  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: C1000765  
; CURRENT APPLICATION NUMBER: US/60/230,445  
; CURRENT FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 3051  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1642  
; LENGTH: 588  
; TYPE: PRT  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(588)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-60-230-445-1642

Query Match 90.7%; Score 2580.5; DB 27; Length 588;  
Best Local Similarity 87.6%; Pred. No. 1.7e-232;  
Matches 514; Conservative 2; Mismatches 10; Indels 61; Gaps 2;

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1 MRDYDEVIAFLGEMGPORLIFFLLSASTIPNGFNKSVYFLAGTPBEHRCRVDPANLSS 60  
|  
61 AMRNNVPLRLDGRVPHSCSRVRLATTANFSALGLEPGRVDLQGLEQSCLDGWERS 120  
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61 AMRNNVPLRLDGRVPHSCSRVRLATTANFSALGLEPGRVDLQGLEQSCLDGWERS 120  
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121 QDYVLSVTVTEEMNLVCDNNKVPPLTSLFFVGVLLGSFVSQGLSDRGRKNVLPATMAVO 180  
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121 QDYVLSVTVTEEMNLVCDNNKVPPLTSLFFVGVLLGSFVSQGLSDRGRKNVLPATMAVO 180  
|  
181 TGFSEFLQIFSIEMEFVLVIVGMOISNVVAFILGTEILGKSVRIIFSTLGCFFFA 240  
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181 TGFSEFLQIFSIEMEFVLVIVGMOISNVVAFILGTEILGKSVRIIFSTLGCFFFA 240  
|  
241 VGYMLLPFAFVIRDMRMILLALVPGVLCVPLMWFIPESPRMLISQRRFEADIIQKA 300  
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241 VGYMLLPFAFVIRDMRMILLALVPGVLCVPLMWFIPESPRMLISQRRFEADIIQKA 300  
|

Db 301 PLEAFYTRDMRMLLALTPBGLVCLPMLCWFHSLWESVESHGPTQRFRREADIIOK 360  
QY 300 AAKNNNTAVPAVIFDSVEEINPLKOOKAFITLDFPRRNIAIMTISLLMLMTSVGYFAL 359  
Db 361 AAKNNNTAVPAVIFDSVEEINPLKOOKAFITLDFPRRNIAIMTISLLMLMTSVGYFAL 420  
QY 360 SLADAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 419  
Db 421 SLADAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 480  
QY 420 VDYFELSLGLVMLGKRGITSAFSAFMLYVFAELPPLVRMAVGVSTASRGSIITAPYV 479  
Db 481 VDYFELSLGLVMLGKRGITSAFSAFMLYVFAELPPLVRMAVGVSTASRGSIITAPYV 540  
QY 480 YLGAYNRMPLPYIYVMSLTVLIGITLFFPESIGMTLPETLEOKOKYK 526  
Db 541 YLGAYNRMPLPYIYVMSLTVLIGITLFFPESIGMTLPETLEOKOKYK 587  
RESULT 6  
US-09-521-195-22  
Sequence 22, Application US/09521195  
GENERAL INFORMATION:  
APPLICANT: Nezu, Jun-ichi  
TITLE OF INVENTION: TRANSPORTER GENES  
FILE REFERENCE: 06501-057001  
CURRENT APPLICATION NUMBER: US/09/521,195  
CURRENT FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: JP 10/156660  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: JP 9/260972  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: PCT/JP98/04009  
PRIOR FILING DATE: 1998-09-07  
NUMBER OF SEQ ID NOS: 32  
SEQ ID NO 22  
LENGTH: 553  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-521-195-22  
Query Match 86.8%; Score 2470; DB 19; Length 553;  
Best Local Similarity 84.6%; Pred. No. 3,6e-222;  
Matches 468; Conservative 39; Mismatches 44; Indels 2; Gaps 1;  
QY 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVYFAGTPEHRCPVDAANLSS 60  
Db 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVYFAGTPEHRCPVDAANLSS 60  
QY 61 AARNNSVPLRLDGRVPHSCRRYRLATIANFSALGLEPGRVDVLGQLEBESCLDGMERS 120  
Db 61 SMRNHSIPLKTRDGRVPHSCRRYRLATIANFSALGLEPGRVDVLGQLEBESCLDGMERS 120  
QY 121 QDVYLSVTVTEMNLVCEDMNKVPLTTSLEFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
Db 121 KQIFLSTVTEMNLVCEDMNKVPLTTSLEFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
QY 181 TGFSFLOFISISWEMFTVLVIVGGOISNYVAIFLIGTELILKSVRIIFSTIGVCTFFA 240  
Db 181 TGFSFLOFISISWEMFTVLVIVGGOISNYVAIFLIGTELILKSVRIIFSTIGVCTFFA 240  
QY 241 VGYMLPLFAFIRDMRMLLALTPBGLVCLPMLFIPESPRMLISORRFAEDIIOKA 300  
Db 241 IGYVNLPLFAFIRDMRMLLALTPBGLVCLPMLFIPESPRMLISORRFAEDIIOKA 300  
QY 301 AKNNNTAVPAVIFDSVE--ELNPLKOOKAFITLDFRTNRITAMTISLLMLMTSVGYFA 358  
Db 301 AKNNNTAVPAVIFDSVEEINPLKOOKAFITLDFRTNRITAMTISLLMLMTSVGYFA 360  
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 418  
Db 361 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 420

QY 419 PVDYFELSLGLVMLGKRGITSAFSAFMLYVFAELPPLVRMAVGVSTASRGSIITAPYF 478  
Db 421 PEDYNFVSIGLVMGKRGITSAFSAFMLYVFAELPPLVRMAVGVSTASRGSIITAPYF 480  
QY 479 YVLGAYNRMPLPYIYVMSLTVLIGITLFFPESIGMTLPETLEOKOKYKVFPSGKTRSM 538  
Db 481 YVLGAYNRMPLPYIYVMSLTVLIGITLFFPESIGMTLPETLEOKOKYKVFPSGKTRSM 540  
QY 539 ETEENPKVLTIAF 551  
Db 541 DREESPKVLTIAF 553  
RESULT 7  
US-09-521-195b-22  
Sequence 22, Application US/09521195b  
GENERAL INFORMATION:  
APPLICANT: Nezu, Jun-ichi  
TITLE OF INVENTION: TRANSPORTER GENES  
FILE REFERENCE: 06501-057001  
CURRENT APPLICATION NUMBER: US/09/521,195b  
CURRENT FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: JP 10/156660  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: JP 9/260972  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: PCT/JP98/04009  
PRIOR FILING DATE: 1998-09-07  
NUMBER OF SEQ ID NOS: 33  
SEQ ID NO 22  
LENGTH: 553  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-521-195b-22  
Query Match 86.8%; Score 2470; DB 19; Length 553;  
Best Local Similarity 84.6%; Pred. No. 3,6e-222;  
Matches 468; Conservative 39; Mismatches 44; Indels 2; Gaps 1;  
QY 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVYFAGTPEHRCPVDAANLSS 60  
Db 1 MRDYDEVIAFLGEMGFORLIFELLASIIIPNGFNGMSVYFAGTPEHRCPVDAANLSS 60  
QY 61 AARNNSVPLRLDGRVPHSCRRYRLATIANFSALGLEPGRVDVLGQLEBESCLDGMERS 120  
Db 61 SMRNHSIPLKTRDGRVPHSCRRYRLATIANFSALGLEPGRVDVLGQLEBESCLDGMERS 120  
QY 121 QDVYLSVTVTEMNLVCEDMNKVPLTTSLEFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
Db 121 KQIFLSTVTEMNLVCEDMNKVPLTTSLEFVGVLLGSFVSGQLSDRGRKNVLFATMAVQ 180  
QY 181 TGFSFLOFISISWEMFTVLVIVGGOISNYVAIFLIGTELILKSVRIIFSTIGVCTFFA 240  
Db 181 TGFSFLOFISISWEMFTVLVIVGGOISNYVAIFLIGTELILKSVRIIFSTIGVCTFFA 240  
QY 241 VGYMLPLFAFIRDMRMLLALTPBGLVCLPMLFIPESPRMLISORRFAEDIIOKA 300  
Db 241 IGYVNLPLFAFIRDMRMLLALTPBGLVCLPMLFIPESPRMLISORRFAEDIIOKA 300  
QY 301 AKNNNTAVPAVIFDSVE--ELNPLKOOKAFITLDFRTNRITAMTISLLMLMTSVGYFA 358  
Db 301 AKNNNTAVPAVIFDSVEEINPLKOOKAFITLDFRTNRITAMTISLLMLMTSVGYFA 360  
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 418  
Db 361 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRTLPRIYIAAVLFWGGVLLFTQIOLV 420  
QY 419 PVDYFELSLGLVMLGKRGITSAFSAFMLYVFAELPPLVRMAVGVSTASRGSIITAPYF 478  
Db 421 PEDYNFVSIGLVMGKRGITSAFSAFMLYVFAELPPLVRMAVGVSTASRGSIITAPYF 480

OY 479 VYGAAYNMLPYIYVMSLVLIGITLFFPESLGMITPETLEOMOKVWFRSGKTRDSM 538  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
DB 481 VYGAAYNMLPYIYVMSLVLIGITLFFPESLGMITPETLEOMOKVWFRSGKTRDSM 540  
OY 539 ETEENPKVLITAF 551  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 541 DRESPEKVLITAF 553

## RESULT 8

US-60-230-445-1548  
; Sequence 1548, Application US/60230445  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: C1000765  
; CURRENT APPLICATION NUMBER: US/60/230,445  
; CURRENT FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 3051  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1548  
; LENGTH: 616  
; TYPE: PRP  
; ORGANISM: HUMAN  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(616)  
; OTHER INFORMATION: Xaa - Any Amino Acid  
US-60-230-445-1548

Query Match 86.3%; Score 2454.5; DB 27; Length 616;

Best Local Similarity 81.0%; Pred. No. 1.2e-220; Indels 89; Gaps 3;  
Matches 498; Conservative 7; Mismatches 21;

OY 1 MRDYEVIATLGEWGFQRLIFLLSASITPNGFNGMSVFLAGTPRRCRVDPANLSS 60  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 1 MRDYEVIATLGEWGFQRLIFLLSASITPNGFNGMSVFLAGTPRRCRVDPANLSS 60  
OY 61 AMRNSVPLRLDGRVPHSCSRRLATIANFSALGLEPRVDYDGLQLESCLDGWEFS 120  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 61 AMRNSVPLRLDGRVPHSCSRRLATIANFSALGLEPRVDYDGLQLESCLDGWEFS 120  
OY 121 ODVYLSVTYTE----- 131  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 121 ODVYLSVTYTEHKKNGSSYLGYGQENTVLSPIFGRAATAHOGOPMPHPDSLYSL 180  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 132 -----NNLVC-EDNMKVPLTTSLEFVGVLGSGF 158  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 181 SKPOKELRYAQRGEITIOKNVNLKSPQERTLFEIECVKQPKALKNGBEFSGVLLGSF 240  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 159 VSGOLSDRGRKKNVLFATMAVQTFSLQTFISWEMFTVLFVIVGQOISNYVAFITLG 218  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 241 VSGOLSDRGRKKNVLFATMAVQTFSLQTFISWEMFTVLFVIVGQOISNYVAFITLG 300  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 219 TELIGKSVRIITFTLGVCTFFAVGYMLLPFAFIRDMRMILLATVPGVLCVPLMFEIP 278  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 301 TELIGKSVRIITFTLGVCTFFAVGYMLLPFAFIRDMRMILLATVPGVLCVPLMFEIP 360  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 279 ESPRWL-----SQRFRFRAEDIIKAAKMNNTAVPAVTFDSVEEINPLKQKAFILD 331  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 361 HSLIWESVESHGPFQRRFRAEDIIKAAKMNNTAVPAVTFDSVEEINPLKQKAFILD 420  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 332 LFRIRNIAIMTMSLMLMTSVGFALSLDAPNHLGDAYNCFLSALIEIPATITAML 391  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 421 LFRIRNIAIMTMSLMLMTSVGFALSLDAPNHLGDAYNCFLSALIEIPATITAML 480  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 392 LRTTPRRYIIAAVLFWMGGVLLFQIOLVVDYFSLIGIVMLGKFGITSFAGMLVYFAEL 451  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 481 LRTTPRRYIIAAVLFWMGGVLLFQIOLVVDYFSLIGIVMLGKFGITSFAGMLVYFAEL 540  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 452 YPTLVNMAVGVTSASRVGSIAPYFYVLYGAYNMLPYIYVMSLVLIGITLFFPESL 511  
| | | | | : | | | | | : | | | | | : | | | | | :

DB 541 YPTLVNMAVGVTSASRVGSIAPYFYVLYGAYNMLPYIYVMSLVLIGITLFFPESL 600  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 512 GMTLPETLEOMOKYK 526  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 601 GMTLPETLEOMOKYK 615

## RESULT 9

US-60-230-445-1385  
; Sequence 1385, Application US/60230445  
; GENERAL INFORMATION:  
; APPLICANT: Beasley, Ellen  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: C1000765  
; CURRENT APPLICATION NUMBER: US/60/230,445  
; CURRENT FILING DATE: 2000-09-06  
; NUMBER OF SEQ ID NOS: 3051  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1385  
; LENGTH: 527  
; TYPE: PRP  
; ORGANISM: HUMAN  
US-60-230-445-1385

Query Match 79.0%; Score 2247; DB 27; Length 527;

Best Local Similarity 77.2%; Pred. No. 2.8e-201; Indels 122; Gaps 3;  
Matches 454; Conservative 2; Mismatches 10;

OY 1 MRDYEVIATLGEWGFQRLIFLLSASITPNGFNGMSVFLAGTPRRCRVDPANLSS 60  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 1 MRDYEVIATLGEWGFQRLIFLLSASITPNGFNGMSVFLAGTPRRCRVDPANLSS 60  
OY 61 AMRNSVPLRLDGRVPHSCSRRLATIANFSALGLEPRVDYDGLQLESCLDGWEFS 120  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 61 AMRNSVPLRLDGRVPHSCSRRLATIANFSALGLEPRVDYDGLQLESCLDGWEFS 120  
OY 121 ODVYLSVTYTE----- 131  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 121 ODVYLSVTYTEHKKNGSSYLGYGQENTVLSPIFGRAATAHOGOPMPHPDSLYSL 180  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 132 -----NNLVCEDNMKVPLTTSLEFVGVLGSGFVSGOLSDRGRKKNVLFATMAVQTFSL 186  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 181 SKPOKKNIVCEDNMKVPLTTSLEFVGVLGSGFVSGOLSDRGRKKNVLFATMAVQTFSL 240  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 187 QIFISWEMFTVLFVIVGQOISNYVAFITLGLTIGKSVRIITFTLGVCTFFAVGYMLL 246  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 241 QIFISWEMFTVLFVIVGQOISNYVAFITLGLTIGKSVRIITFTLGVCTFFAVGYMLL 300  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 247 PLFAFIRDMRMILLATVPGVLCVPLMFEIPESRWL-----SQRFRFRAEDIIK 299  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 301 PLFAFIRDMRMILLATVPGVLCVPLMFEIPESRWL-----SQRFRFRAEDIIK 360  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 300 AAKMNNTAVPAVTFDSVEEINPLKQKAFILDIFRTNIAIMTMSLMLTSGYFAL 359  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 361 AAKMNNTAVPAVTFDSVEEINPLKQKAFILDIFRTNIAIMTMSLMLTSGYFAL 420  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 360 SLDAPNHLGDAYNCFLSALIEIPATITAMLRTLPRIYIIAAVLFWMGGVLLFQIOLV 419  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 421 SLDAPNHLGDAYNCFLSALIEIPATITAMLRTLPRIYIIAAVLFWMGGVLLFQIOLV 480  
| | | | | : | | | | | : | | | | | : | | | | | :  
OY 420 VDYFSLIGIVMLGKFGITSFAGMLVYFAELYPTLVNMAVGVTSASRVGSIAPYFV 479  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 481 V----- 481

## RESULT 10

OY 480 YLGAAYNMLPYIYVMSLVLIGITLFFPESLGMITPETLEOMOKYK 527  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 482 --GAYNMLPYIYVMSLVLIGITLFFPESLGMITPETLEOMOKYK 527  
| | | | | : | | | | | : | | | | | : | | | | | :

PCT-US01-08631-33388  
; Sequence 33388, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 33388  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (428)..(478)  
; OTHER INFORMATION: Sugar transport proteins domain identified by eMATRIX,  
; OTHER INFORMATION: accession number BL00216b, p-value=4.375e-11, raw score of 27.64  
; NAME/KEY: DOMAIN  
; LOCATION: (108)..(525)  
; OTHER INFORMATION: Sugar (and other) transporter domain identified by Pfam,  
; OTHER INFORMATION: accession name sugar\_tr, E-value=5.6e-08, Pfam score of 32.9  
PCT-US01-08631-33388

Query Match 78.0%; Score 2218; DB 1; Length 557;  
Best Local Similarity 75.9%; Pred. No. 1.6e-198;  
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

QY 1 MRDDEVIAFLGEMGFQRLIFFLSASTIPNGFMSVFLAGTPEHRCVPDANLSS 60  
DB 1 MRDDEVIAFLGEMGFQRLIFFLSASTIPNGFMSVFLAGTPEHRCVPDANLSS 60  
QY 61 AMRNNVPLRLRGREVPSCSRRLATIANFSALGLEGRVDIGOLEQESCLDGMFES 120  
DB 61 AMRNNVPLRLRGREVPSCSRRLATIANFSALGLEGRVDIGOLEQESCLDGMFES 120  
QY 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
DB 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
QY 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
DB 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
QY 181 TGFSFLQIFSIWEMFTVLFIYGMQISNYVAFLGTETLIGKSVRIIFSTLGCYFEA 240  
DB 181 TGFSFLQIFSIWEMFTVLFIYGMQISNYVAFLGTETLIGKSVRIIFSTLGCYFEA 240  
QY 241 VGYMLPLRAYFRDMRMLLALTVPVCVPLMWFIPSPRMLISQGRFEAEVITRKA 300  
DB 241 VGYMLPLRAYFRDMRMLLALTVPVCVPLMWFIPSPRMLISQGRFEAEVITRKA 300  
QY 301 AKANNTPAVPAVIED--SVEELNPLKQOKAFIIDLFTFRNIAIMTMSLLMMLTSVGYFA 358  
DB 301 AKANNTPAVPAVIED--SVEELNPLKQOKAFIIDLFTFRNIAIMTMSLLMMLTSVGYFA 358  
QY 301 AKANGIYVPTIFDPSLQDLSKKQOSHNIIDLRTWNIHVTIMSLMWTISVGYFG 360  
DB 301 AKANGIYVPTIFDPSLQDLSKKQOSHNIIDLRTWNIHVTIMSLMWTISVGYFG 360  
QY 359 LSLDAPNLGDAFLNCLSLALFIIPAYITAMLLKTLPRRYITAAVLEFGGVLLFIQV 418  
DB 359 LSLDAPNLGDAFLNCLSLALFIIPAYITAMLLKTLPRRYITAAVLEFGGVLLFIQV 418  
QY 361 LSLDTPMLHGDIVNCFLSAMVEVPAYVLAAMLLQYLPFRYSMAALFLGSGVLLFMQV 420  
DB 361 LSLDTPMLHGDIVNCFLSAMVEVPAYVLAAMLLQYLPFRYSMAALFLGSGVLLFMQV 420  
QY 419 PVDYFELSLGLVMGKGTSAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 478  
DB 419 PVDYFELSLGLVMGKGTSAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 478  
QY 421 PPDLYIATVAVVAGFGVTAFAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 480  
DB 421 PPDLYIATVAVVAGFGVTAFAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 480  
QY 479 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 535  
DB 479 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 535  
QY 481 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 540  
DB 481 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 540  
QY 536 DSMETENPKVL--ITAF 551  
DB 536 DSMETENPKVL--ITAF 551  
QY 541 MKDGOERPTILKSTAF 557  
DB 541 MKDGOERPTILKSTAF 557

RESULT 11  
PCT-US02-17382-202  
; Sequence 202, Application PC/TUS0217382  
; GENERAL INFORMATION:  
; APPLICANT: EXELTIS, INC.  
; TITLE OF INVENTION: MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
; FILE REFERENCE: EX02-062  
; CURRENT APPLICATION NUMBER: PCT/US02/17382  
; PRIOR FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/357,253  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 234  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 202  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US02-17382-202

Query Match 78.0%; Score 2218; DB 1; Length 557;  
Best Local Similarity 75.9%; Pred. No. 1.6e-198;  
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

QY 1 MRDDEVIAFLGEMGFQRLIFFLSASTIPNGFMSVFLAGTPEHRCVPDANLSS 60  
DB 1 MRDDEVIAFLGEMGFQRLIFFLSASTIPNGFMSVFLAGTPEHRCVPDANLSS 60  
QY 61 AMRNNVPLRLRGREVPSCSRRLATIANFSALGLEGRVDIGOLEQESCLDGMFES 120  
DB 61 AMRNNVPLRLRGREVPSCSRRLATIANFSALGLEGRVDIGOLEQESCLDGMFES 120  
QY 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
DB 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
QY 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
DB 121 ODVYLSIVTENNLCVEDMKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLEVTGMQ 180  
QY 181 TGFSFLQIFSIWEMFTVLFIYGMQISNYVAFLGTETLIGKSVRIIFSTLGCYFEA 240  
DB 181 TGFSFLQIFSIWEMFTVLFIYGMQISNYVAFLGTETLIGKSVRIIFSTLGCYFEA 240  
QY 241 VGYMLPLRAYFRDMRMLLALTVPVCVPLMWFIPSPRMLISQGRFEAEVITRKA 300  
DB 241 VGYMLPLRAYFRDMRMLLALTVPVCVPLMWFIPSPRMLISQGRFEAEVITRKA 300  
QY 301 AKANNTPAVPAVIED--SVEELNPLKQOKAFIIDLFTFRNIAIMTMSLLMMLTSVGYFA 358  
DB 301 AKANNTPAVPAVIED--SVEELNPLKQOKAFIIDLFTFRNIAIMTMSLLMMLTSVGYFA 358  
QY 301 AKANGIYVPTIFDPSLQDLSKKQOSHNIIDLRTWNIHVTIMSLMWTISVGYFG 360  
DB 301 AKANGIYVPTIFDPSLQDLSKKQOSHNIIDLRTWNIHVTIMSLMWTISVGYFG 360  
QY 359 LSLDAPNLGDAFLNCLSLALFIIPAYITAMLLKTLPRRYITAAVLEFGGVLLFIQV 418  
DB 359 LSLDAPNLGDAFLNCLSLALFIIPAYITAMLLKTLPRRYITAAVLEFGGVLLFIQV 418  
QY 361 LSLDTPMLHGDIVNCFLSAMVEVPAYVLAAMLLQYLPFRYSMAALFLGSGVLLFMQV 420  
DB 361 LSLDTPMLHGDIVNCFLSAMVEVPAYVLAAMLLQYLPFRYSMAALFLGSGVLLFMQV 420  
QY 419 PVDYFELSLGLVMGKGTSAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 478  
DB 419 PVDYFELSLGLVMGKGTSAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 478  
QY 421 PPDLYIATVAVVAGFGVTAFAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 480  
DB 421 PPDLYIATVAVVAGFGVTAFAFSAFMYFTAEIYPLVNNMAVGYTASRAGSTIAYF 480  
QY 479 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 535  
DB 479 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 535  
QY 481 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 540  
DB 481 VYLGAVYRMLPYIVMGSFLVLIIGITLFPESLGMTLPETLQOKVWFRSGK---KTR 540  
QY 536 DSMETENPKVL--ITAF 551  
DB 536 DSMETENPKVL--ITAF 551  
QY 541 MKDGOERPTILKSTAF 557  
DB 541 MKDGOERPTILKSTAF 557

RESULT 12  
PCT-US02-17456-39  
; Sequence 39, Application PC/TUS0217456  
; GENERAL INFORMATION:



PRIOR APPLICATION NUMBER: PCT/JP98/04009  
PRIOR FILING DATE: 1998-09-07  
NUMBER OF SEQ ID NOS: 32  
SEQ ID NO 3  
LENGTH: 557  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-521-195-3

Query Match 78.0%; Score 2218; DB 19; Length 557;  
Best Local Similarity 75.9%; Pred. No. 1.6e-198;  
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

QY 1 MRDDEVIAFLGEMGFQRLIFLLSASIIIPNGFNMSVYELAGTPHRCRVPDAANLSS 60  
DB 1 MRDDEVIAFLGEMGFQRLIFLLSASIIIPNGFNMSVYELAGTPHRCRVPDAANLSS 60  
QY 61 AMRNNSVPLRLRDGREVPHSCRRYRATIANFSALEPGRDVDLGOLEQESCLDGWERS 120  
DB 61 AMRNHVPRLRLRDGREVPHSCRRYRATIANFSALEPGRDVDLGOLEQESCLDGWERS 120  
QY 121 ODVYLSVTYEMNLVCEDMKAPLITSLFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180  
DB 121 ODVYLSVTYEMNLVCEDMKAPLITSLFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180  
QY 181 TGFSEFLQISISWEMFTVLFYVGMQISNYVAFLGTETELGKSVRIIFSTLGCYCFYA 240  
DB 181 TGFSEFLQISISWEMFTVLFYVGMQISNYVAFLGTETELGKSVRIIFSTLGCYCFYA 240  
QY 241 VGYMLPLFAFIRDMRMLLALTVPGVLCVPLMFIPESPRMLISGRFREAEDIIQKA 300  
DB 241 VGYMLPLFAFIRDMRMLLALTVPGVLCVPLMFIPESPRMLISGRFREAEDIIQKA 300  
QY 301 AKNNTAVPAVIFD--SVEELNPLKQOKAFILDFRTNIAINTMSLLMLNLSVGYFA 358  
DB 301 AKANGIVPSTIFDESELODLSKKQOSHNIIDLRTWNRMTYIMTISVGYFG 360  
QY 359 LSLDAPNLGDAYLNCFLSALIEIPAYITAMLLRTLPRTYITIAVLFMGVLLFIOLV 418  
DB 359 LSLDAPNLGDAYLNCFLSALIEIPAYITAMLLRTLPRTYITIAVLFMGVLLFIOLV 418  
QY 421 PPDLYLATVAVLWVGKGVTAASMYVYTAELPTVVRNMGVGSSTASRLSISPYF 480  
DB 421 PPDLYLATVAVLWVGKGVTAASMYVYTAELPTVVRNMGVGSSTASRLSISPYF 480  
QY 479 VYLGAVNRMLPYIVGSLTVLIGITLFFPESLGMTLPETLEQMKVWFRSGK---KTR 535  
DB 479 VYLGAVNRMLPYIVGSLTVLIGITLFFPESLGMTLPETLEQMKVWFRSGK---KTR 535  
QY 536 DSMETENPKVL-ITAF 551  
DB 541 MKDQGERPTILKSTAF 557

RESULT 15  
US-09-521-195b-3  
Sequence 3, Application US/09521195B  
GENERAL INFORMATION:  
APPLICANT: Nezu, Jun-ichi  
APPLICANT: Oku, Asuka  
TITLE OF INVENTION: TRANSPORTER GENES  
FILE REFERENCE: 06501-057001  
CURRENT APPLICATION NUMBER: US/09/521.195B  
CURRENT FILING DATE: 2000-03-07  
PRIOR APPLICATION NUMBER: JP 10/156660  
PRIOR FILING DATE: 1998-05-20  
PRIOR APPLICATION NUMBER: JP 9/260972  
PRIOR FILING DATE: 1997-09-08  
PRIOR APPLICATION NUMBER: PCT/JP98/04009  
PRIOR FILING DATE: 1998-09-07  
NUMBER OF SEQ ID NOS: 33  
SEQ ID NO 3  
LENGTH: 557

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-521-195b-3

Query Match 78.0%; Score 2218; DB 19; Length 557;  
Best Local Similarity 75.9%; Pred. No. 1.6e-198;  
Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;

QY 1 MRDDEVIAFLGEMGFQRLIFLLSASIIIPNGFNMSVYELAGTPHRCRVPDAANLSS 60  
DB 1 MRDDEVIAFLGEMGFQRLIFLLSASIIIPNGFNMSVYELAGTPHRCRVPDAANLSS 60  
QY 61 AMRNNSVPLRLRDGREVPHSCRRYRATIANFSALEPGRDVDLGOLEQESCLDGWERS 120  
DB 61 AMRNHVPRLRLRDGREVPHSCRRYRATIANFSALEPGRDVDLGOLEQESCLDGWERS 120  
QY 121 ODVYLSVTYEMNLVCEDMKAPLITSLFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180  
DB 121 ODVYLSVTYEMNLVCEDMKAPLITSLFVGVLLGSFVSGQLSDRFGRKNVLFATMAVQ 180  
QY 181 TGFSEFLQISISWEMFTVLFYVGMQISNYVAFLGTETELGKSVRIIFSTLGCYCFYA 240  
DB 181 TGFSEFLQISISWEMFTVLFYVGMQISNYVAFLGTETELGKSVRIIFSTLGCYCFYA 240  
QY 241 VGYMLPLFAFIRDMRMLLALTVPGVLCVPLMFIPESPRMLISGRFREAEDIIQKA 300  
DB 241 VGYMLPLFAFIRDMRMLLALTVPGVLCVPLMFIPESPRMLISGRFREAEDIIQKA 300  
QY 301 AKNNTAVPAVIFD--SVEELNPLKQOKAFILDFRTNIAINTMSLLMLNLSVGYFA 358  
DB 301 AKANGIVPSTIFDESELODLSKKQOSHNIIDLRTWNRMTYIMTISVGYFG 360  
QY 359 LSLDAPNLGDAYLNCFLSALIEIPAYITAMLLRTLPRTYITIAVLFMGVLLFIOLV 418  
DB 359 LSLDAPNLGDAYLNCFLSALIEIPAYITAMLLRTLPRTYITIAVLFMGVLLFIOLV 418  
QY 421 PPDLYLATVAVLWVGKGVTAASMYVYTAELPTVVRNMGVGSSTASRLSISPYF 480  
DB 421 PPDLYLATVAVLWVGKGVTAASMYVYTAELPTVVRNMGVGSSTASRLSISPYF 480  
QY 479 VYLGAVNRMLPYIVGSLTVLIGITLFFPESLGMTLPETLEQMKVWFRSGK---KTR 535  
DB 479 VYLGAVNRMLPYIVGSLTVLIGITLFFPESLGMTLPETLEQMKVWFRSGK---KTR 535  
QY 536 DSMETENPKVL-ITAF 551  
DB 541 MKDQGERPTILKSTAF 557

Search completed: July 3, 2003, 12:41:39  
Job time : 152 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2003, 12:37:45 ; Search time 25 Seconds

(without alignments)  
2534.444 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845

Sequence: 1 MRDYDEVIAFLGEMGPPORL.....KTRDSMETEENKVLITAF 551

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 440863 seqs, 114992915 residues

Total number of hits satisfying chosen parameters: 440863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubppaa/PTCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*  
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8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*  
10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep:\*  
12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                   | Description         |
|------------|-------|-------------|--------|----------------------|---------------------|
| 1          | 2218  | 78.0        | 557    | 10 US-09-798-743A-1  | Sequence 1, App1    |
| 2          | 2164  | 76.1        | 557    | 10 US-09-798-743A-3  | Sequence 3, App1    |
| 3          | 691.5 | 24.3        | 556    | 9 US-09-284-320-83   | Sequence 83, App1   |
| 4          | 685.5 | 24.1        | 554    | 9 US-09-284-320-5    | Sequence 5, App1    |
| 5          | 654.5 | 23.0        | 547    | 9 US-10-155-891-2    | Sequence 2, App1    |
| 6          | 641   | 22.5        | 476    | 9 US-10-155-891-4    | Sequence 4, App1    |
| 7          | 625.5 | 22.0        | 553    | 9 US-10-095-139-5    | Sequence 5, App1    |
| 8          | 599   | 21.1        | 553    | 9 US-10-095-139-17   | Sequence 17, App1   |
| 9          | 586   | 20.6        | 550    | 9 US-10-086-816A-2   | Sequence 2, App1    |
| 10         | 564   | 19.8        | 550    | 9 US-10-095-139-16   | Sequence 16, App1   |
| 11         | 564   | 19.8        | 550    | 9 US-10-339-513-2    | Sequence 2, App1    |
| 12         | 398   | 14.0        | 572    | 10 US-09-919-781-2   | Sequence 2, App1    |
| 13         | 303.5 | 10.7        | 448    | 9 US-09-738-626-6795 | Sequence 6795, App1 |
| 14         | 280   | 9.8         | 486    | 10 US-09-860-232A-7  | Sequence 7, App1    |
| 15         | 276.5 | 9.7         | 488    | 9 US-10-170-528-5    | Sequence 5, App1    |
| 16         | 276.5 | 9.7         | 488    | 9 US-10-062-960B-4   | Sequence 4, App1    |
| 17         | 276.5 | 9.7         | 488    | 9 US-10-162-012-46   | Sequence 46, App1   |
| 18         | 276.5 | 9.7         | 488    | 9 US-10-144-624-4    | Sequence 4, App1    |
| 19         | 276.5 | 9.7         | 488    | 12 US-10-094-059-4   | Sequence 4, App1    |

|    |       |     |     |                       |                     |
|----|-------|-----|-----|-----------------------|---------------------|
| 20 | 275.5 | 9.7 | 487 | 9 US-10-095-139-14    | Sequence 14, App1   |
| 21 | 275.5 | 9.7 | 487 | 9 US-10-156-239-27    | Sequence 27, App1   |
| 22 | 275.5 | 9.7 | 487 | 9 US-10-199-485-27    | Sequence 27, App1   |
| 23 | 275.5 | 9.7 | 487 | 10 US-09-795-693-27   | Sequence 2, App1    |
| 24 | 267   | 9.4 | 520 | 9 US-10-000-273-2     | Sequence 2, App1    |
| 25 | 266.5 | 9.4 | 535 | 9 US-10-156-239-20    | Sequence 20, App1   |
| 26 | 266.5 | 9.4 | 535 | 9 US-10-139-485-20    | Sequence 20, App1   |
| 27 | 266.5 | 9.4 | 535 | 10 US-09-795-693-20   | Sequence 20, App1   |
| 28 | 247   | 8.7 | 530 | 9 US-09-991-936-1902  | Sequence 1902, App1 |
| 29 | 246.5 | 8.7 | 490 | 9 US-10-128-714-8149  | Sequence 8149, App1 |
| 30 | 244.5 | 8.6 | 727 | 9 US-10-170-528-4     | Sequence 4, App1    |
| 31 | 244.5 | 8.6 | 727 | 10 US-09-822-246-4    | Sequence 4, App1    |
| 32 | 243   | 8.5 | 431 | 9 US-09-738-626-6797  | Sequence 4697, App1 |
| 33 | 240.5 | 8.5 | 469 | 9 US-10-156-761-9834  | Sequence 9834, App1 |
| 34 | 239   | 8.4 | 480 | 9 US-10-176-847-76    | Sequence 76, App1   |
| 35 | 237.5 | 8.3 | 727 | 10 US-09-822-246-2    | Sequence 2, App1    |
| 36 | 237   | 8.3 | 474 | 9 US-10-128-714-8149  | Sequence 3149, App1 |
| 37 | 234.5 | 8.2 | 494 | 9 US-09-981-947A-5    | Sequence 5, App1    |
| 38 | 234   | 8.2 | 405 | 10 US-09-972-724-5    | Sequence 36, App1   |
| 39 | 234   | 8.2 | 553 | 9 US-10-051-909-16    | Sequence 48, App1   |
| 40 | 233   | 8.2 | 501 | 10 US-09-778-927A-48  | Sequence 47, App1   |
| 41 | 227   | 8.0 | 471 | 10 US-09-778-927A-47  | Sequence 5079, App1 |
| 42 | 224.5 | 7.9 | 451 | 10 US-09-815-242-5079 | Sequence 160, App1  |
| 43 | 219   | 7.7 | 742 | 9 US-09-374-046A-160  | Sequence 10, App1   |
| 44 | 216   | 7.6 | 493 | 9 US-09-981-947A-160  | Sequence 22, App1   |
| 45 | 216   | 7.6 | 510 | 9 US-10-051-902-22    | Sequence 22, App1   |

## ALIGNMENTS

|   |     |   |  |  |  |
|---|-----|---|--|--|--|
| RESULT 1  |     |   |  |  |  |
| US-09-798-743A-1  |     |   |  |  |  |
| ; Sequence 1, Application US/09798743A                                    |     |   |  |  |  |
| ; Patent No. US2002009903A1   |     |   |  |  |  |
| ; GENERAL INFORMATION:  |     |   |  |  |  |
| ; APPLICANT: Nezu, Jun-ichi   |     |   |  |  |  |
| ; TITLE OF INVENTION: SYSTEMIC CARNITINE DEFICIENCY GENE AND USES THEREOF |     |   |  |  |  |
| ; FILE REFERENCE: 06501-073001  |     |   |  |  |  |
| ; CURRENT APPLICATION NUMBER: US/09/798,743A                              |     |   |  |  |  |
| ; CURRENT FILING DATE: 2001-03-02   |     |   |  |  |  |
| ; PRIOR APPLICATION NUMBER: PCT/JP99/04853                                |     |   |  |  |  |
| ; PRIOR FILING DATE: 1999-09-07   |     |   |  |  |  |
| ; PRIOR APPLICATION NUMBER: JP 10-252683                                  |     |   |  |  |  |
| ; NUMBER OF SEQ ID NOS: 31  |     |   |  |  |  |
| ; SOFTWARE: PatentIn Ver. 2.0   |     |   |  |  |  |
| ; SEQ ID NO 1   |     |   |  |  |  |
| ; LENGTH: 557   |     |   |  |  |  |
| ; TYPE: PRT   |     |   |  |  |  |
| ; ORGANISM: Homo sapiens  |     |   |  |  |  |
| US-09-798-743A-1  |     |   |  |  |  |
| Query Match   |     |   |  |  |  |
| Best Local Similarity 75.9%; Pred. No. 2.4e-182;                          |     |   |  |  |  |
| Matches 423; Conservative 57; Mismatches 71; Indels 6; Gaps 3;            |     |   |  |  |  |
| OY  | 1   | MRDYDEVIAFLGEMGPPORLIFPFLISASITINGNMSVFLAGTPHRCRVDAANLSS 60 |  |  |  |
| DB  | 1   | MRDYDEVIAFLGEMGPPORLIFPFLISASITINGNMSVFLATPHRCRVDAANLSS 60  |  |  |  |
| OY  | 61  | AMRNNSVPLRLDGEVPHSCSRVRLATIANFSLGLEPGDVLGOLDESCIDGMEFS 120  |  |  |  |
| DB  | 61  | AMRNNSVPLRLDGEVPHSCSRVRLATIANFSLGLEPGDVLGOLDESCIDGMEFS 120  |  |  |  |
| OY  | 121 | QDVYLVVTEENLVCEENKVPVLTSLFEVGLISFVSQSLDRGRNVLPATMAVO 180    |  |  |  |
| DB  | 121 | QDVYLVVTEENLVCEENKVPVLTSLFEVGLISFVSQSLDRGRNVLPATMAVO 180    |  |  |  |
| OY  | 181 | TGFSFLQIFSIEMKFTLVYVGQISNVVAFITGTEILGKSVRIITSTLGVCYFEFA 240 |  |  |  |
| DB  | 181 | TGFSFLQIFSIEMKFTLVYVGQISNVVAFITGTEILGKSVRIITSTLGVCYFEFA 240 |  |  |  |



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Db 338 LRTPLRKHFTVILMTMFSCAVLYGGLIMHGATGANLXLDFFVSSLEFPADLILVT 397
OY 392 LRTPLRKHFTVILMTMFSCAVLYGGLIMHGATGANLXLDFFVSSLEFPADLILVT 451
Db 398 IDRIHGYIAVNVAVTSTASRVGSIITAPYFY-LGAYNRMALPYIYMGSLTVLIGITLPPES 510
OY 452 YFTLVNMAVGVTSASRVGSIITAPYFY-LGAYNRMALPYIYMGSLTVLIGITLPPES 510
Db 458 YFTLVNMAVGVTSASRVGSIITAPYFY-LGAYNRMALPYIYMGSLTVLIGITLPPES 517
OY 511 LKMTLPETLEQOKV 525
Db 518 KGVALPETLEAENL 532

RESULT 4
US-09-284-320-5
; Sequence 5, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705CPUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/J97/04056
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-284-320-5

Query Match
Best Local Similarity 33.0%; Score 685.5; DB 9; Length 554;
Matches 190; Conservative 87; Mismatches 229; Indels 69; Gaps 14;

OY 1 MDYDEVIAFLGEMWPFQR--LIFELLASIIIPNGMGSVFLAGTPEHRCRVPDAN 57
Db 1 MFTVDILIOVGESEGMFOKQAFLLICLLSAFAP--ICVGIYFLGFPDHHQSGPVAE 57
OY 58 LSS--AMR-----NNSVPLRLDREVPHSCSRV-----LATIA-NFSALG 96
Db 58 LSGRCGMSPAELNATVPEGLPAGAFIAGOCRRYEVDMNQSALSCVDPLASLSTRSHLP 117
OY 97 LEPGRVDVLGOLEQESCLDGEWESODVYLSIVTEEMNLVCEEDNMKVPPLTSLFEVGLG 156
Db 118 LEP-----CQDGMVY--DTPGSSIVTEFNIVCADSKMLDLPQSCINAGFFEG 162
OY 157 SFVSQSLSRFRGRKAVLPAITAVYQTFESFLQTSISMETFLVLEVIVMGQISNVYAFI 216
Db 163 SLGVGYFADRFGRKCLLTGYLVNVSGLMAFSPNYSMLFRLQGLVSKGNMAGYT 222
OY 217 LGETLLG-----KSVILFSTLGVCFPAVGYMLPLFVYFIRDMKMLLATLVPGVLCVP 272
Db 223 LITTEVSGSSRTVAILYOMA-----FTVGLVALTGLAYALPHMWMQLAVSLPTEFL 277
OY 273 LMFIPESRMLISQRRREADILQAKAKNNNTAVPAVI-----FDSVEELNPKOOK 326
Db 278 YVMCVPESRMLISQRRTEAIKIMDHTAOKNGKLPADIMKLSLEDEYTERKSP----- 332
OY 327 ATILDFRTNIAITFISLLIMLTSGYFALSIDAPNLHGDAYLNCFLSALLEIPAYI 386
Db 333 -SFALFRTPLRKHFTVILMTMFSDVLYGGLIMHGATSGNLTIDFLYSALVEIPGAF 391
OY 387 TMLLRTPLRKHFTVILMTMFSDVLYGGLIMHGATSGNLTIDFLYSALVEIPGAF 446
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Db 392 IALITDVRGRIYPAVSNLLAGAACLMIFISPDLMHNIIMVCGRMGTIAIOMICL 451
OY 447 FTALYPLVNVMAVGVTSASRVGSIITAPYFY-LGAYNRMALPYIYMGSLTVLIGITL 505
Db 452 VNAELYPFVNVNLMVWCSSICLDIGGITTEPVERLEWQALPLILFAVLGLAAGVT 511
OY 506 FEPESLGMTLPETLEQOKVWFRSGKTRDSMT 540
Db 512 LIPETGVALPETMKDAENL-----GRNAKENT 541

RESULT 5
US-10-155-891-2
; Sequence 2, Application US/10155891
; Publication No. US20020193585A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20020193585A1 Human Transporter Proteins and Polynucle
; FILE REFERENCE: LEX-0346-USA
; CURRENT APPLICATION NUMBER: US/10/155,891
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/293,710
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 547
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-155-891-2

Query Match
Best Local Similarity 32.2%; Score 654.5; DB 9; Length 547;
Matches 175; Conservative 86; Mismatches 232; Indels 51; Gaps 9;

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Db 2 EBERAFQAVGMYGTYQMLCFLAVLLQVATEALIALVGAIPSYHM--DLAED--- 55
OY 62 WRNSVPLRLDREVPHSCSRVRLATIANFSALGEPGRVDVLGOLEQESCLDGEWESQ 121
Db 56 -----LPMQSHNGSAGEDQAFG--DMLTANGSETHK 86
OY 122 DVLIS---IVTEEMNLVCEEDNMKVPPLTSLFEVGLLGSFVSQSLDRGRKNVLPATM 177
Db 87 HVHSSSFSTIASSEFLIANRSYKVSAASSFSGVGVYISFGQLSDRGRKKVYLTF 146
OY 178 AVQGFSEFLQTSISMETFLVLEVIVMGQISNVYAFIITGLTELKSVIITSLGVCY 237
Db 147 ALDILFANGFSSYFPAVTRFLVGMNMGSLVAVLLNLCVGTAYMALGSG-GL 205
OY 238 FFAVGYMLPLFAFIFIDMRLALATLVPGVLCVPLMFIPEPRMLISQRRREADII 297
Db 206 FFAVGIAGVALLGVFIRSWRTIALIVNLQTVVFLSLFIPSPRMVYSGRISAEAL 265
OY 298 OKAKANNNTAVPAVIEPDSVEELNPKQKAFIIDLFTNIAITMTNSLLIMLTSGYF 357
Db 266 YLIAKRRKLT--KCTFSLTRPANRSCRETSFIDLFRYVLLGHTLILMTIMFVCSLYY 323
OY 358 ALSIDAPNLHGDAYLNCFLSALLEIPAYIYAFI-----RLPRLRYIAAVLFWGGLVLF 415
Db 324 GLTISAGDLGGSITANIALSGLIETIPYCLITINOKWFGRRRTLSAFCLGGLACTIV 383
OY 416 QLVV-----VDYFISGLVLMKFGITSAFMSLVYFETALYPTLVNMAVGVTSAS 469
Db 384 MLEPEKDTGVFAVNVNHSLSLGLKLTISAAPNIVYITSELPTIYIRNGLGTGMEFR 443
OY 470 VGSIIAFYFYLCAVNMALPYIYMGSLTVLIGITLFFPESLGMTLPETLEQOKVWFR 529
```

Db 444 VGGIAPFIPSLKTVQVMSLPFIVEGATGTLTGILSLPLETLSPLETFESDQVYSYR 503  
QY 530 SGKK 533  
Db 504 LGEE 507

RESULT 6  
US-10-155-891-4

Sequence 4, Application US/10155891  
Publication No. US20020193585A1  
GENERAL INFORMATION:  
APPLICANT: Walke, D. Wade  
APPLICANT: Friddele, Carl Johan  
APPLICANT: Scoville, John  
APPLICANT: Turner, C. Alexander Jr.  
TITLE OF INVENTION: No. US20020193585A1el Human Transporter Proteins and Polynucleoti  
TITLE OF INVENTION: Same  
FILE REFERENCE: LEX-0346-USA  
CURRENT APPLICATION NUMBER: US/10/155,891  
CURRENT FILING DATE: 2002-05-21  
PRIOR APPLICATION NUMBER: US 60/293,710  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 476  
TYPE: PR  
ORGANISM: homo sapiens  
US-10-155-891-4

Query Match 22.5%; Score 641; DB 9; Length 476;  
Best Local Similarity 35.3%; Pred. No. 6.5e-47;  
Matches 159; Conservative 73; Mismatches 190; Indels 28; Gaps 6;

QY 92 FSAIIGERDVLGLOEJSCLDGWEFSDVLYSTVYEMNVCEDNMKVPITSLFV 151  
Db 7 FOAVG-----EMGIYQMTLC-----FLAVLLQWFLIARSRKVSAASSFPS 49  
QY 152 GVLIGSFVSGQLDRFGKKNVLFATMAVQTFGFFLIQISISWEMFTVLFYVGMQISNV 211  
Db 50 GVEVGVISFGQLSDRGKRVYLTGFDLILFALDILFANGFSPSYEFFAVTRFIVGMNGMS 109  
QY 212 VVAFILGETILGKSVRIESTLGVCFPAVGYMLPLFAFIRDMRLALITVPGVLCV 271  
Db 110 LVAFVILNECVGAYMALGSIG-GLFFAVGIAQVALLGYFIRSMRTLAILVMLQGVVF 168  
QY 272 PLWMEIPESPRWLTISORPREADITIOKAKKNNTAVPAVIFDSVEELNPKQKAFITD 331  
Db 169 LLSLFIPEPRWLTISORPREADITIOKAKKNNTAVPAVIFDSVEELNPKQKAFITD 226  
QY 332 LFTRTNIAITMSLLMLTSGVYFALSADAPNLHGDVYLNCFLSALIEIPAYITAMLL 391  
Db 227 LFRYRVLLGHTLILMIFWCVSLVYGLFSLAGDLGSIIYANLALSGLEIPSPICITL 286  
QY 392 L--RTLPKRTIIVAVLEWGGVLLFIQVLP-----VDYFISIGLVMLGKREITAFPM 443  
Db 287 INOKWFGKRTLSAFCLGLACLIWFLPEKRDGVFAVAVNSHSLGLKLTISAENI 346  
QY 444 LVYFETALVPTLVNNAVGTSTASRGTIAPFYVLYGAYNMLPYIWMGLTVLIGIF 503  
Db 347 VYITSTELTYVIRNNGVLCGSMFNRVGGIAPFISLKVQVMSLPFIVEGATGTLTGIL 406  
QY 504 TLEFPESLGMTPELTLEQMKVWFRSGKK 533  
Db 407 SLIPLETLSPLETFESDQVYSYR 436

RESULT 7  
US-10-095-139-5  
Sequence 5, Application US/10095139  
Patent No. US20020165357A1  
GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.  
APPLICANT: Silos-Santiago, Immaculada  
APPLICANT: Millennium Pharmaceuticals, Inc.  
TITLE OF INVENTION: 38554, 57301, and 58324, Human Organic  
TITLE OF INVENTION: Ion Transporters and Uses Therefor  
FILE REFERENCE: MP101-017P1RNM  
CURRENT APPLICATION NUMBER: US/10/095,139  
CURRENT FILING DATE: 2002-03-11  
PRIOR APPLICATION NUMBER: 60/275,172  
PRIOR FILING DATE: 2001-03-12  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 553  
TYPE: PR  
ORGANISM: homo sapiens  
FEATURE:  
OTHER INFORMATION: unknown amino acids at 200-202  
NAME/KEY: VARIANT  
LOCATION: (1)...(553)  
OTHER INFORMATION: Xaa - Any Amino Acid  
US-10-095-139-5

Query Match 22.0%; Score 625.5; DB 9; Length 553;  
Best Local Similarity 30.1%; Pred. No. 1.7e-45;  
Matches 165; Conservative 101; Mismatches 235; Indels 47; Gaps 10;

QY 4 VDEVAFLEGWGPGRILFFLLSIIIPNGFNGSVVLAGTPERCRVP-----DAA 56  
Db 3 FSELDLVGGIGRFVQLQTMALMVSIMMLQSKLENFSAVPSHRAPLLDNTAQA 62  
QY 57 NLSSAMRNNSVPLRLRDG-REVPHSCSYRL-----ATIANFSALGERDVLG 106  
Db 63 ILGSLPALLAISIPBPQNRPHQCRFRPQOMQLDPPNATATWSADREP----- 115  
QY 107 QLEJSCLDGWEFSDVLYSTVYEMNVCEDNMKVPITSLFVGYVILGSGFVSGQLSDR 166  
Db 116 -----CVDGWYDRSIFSTIVAKMNLVCSHALKPMASISYLAGIIVGAACGPASDR 169  
QY 167 FGRKNVL--FATMAVQ--TGSEFLQIFSI-SWEMFTVLFYVGMQISNVYAFILGTEI 221  
Db 170 FGRRLVILWVSYQMAVNGTAFAFAFVYXXRRRLAFHNSGAPLG--LLAVMWTAA 227  
QY 222 LKSVRIITFSTLGVCFPAVGYMLPLFAFIRDMRLALITVPGVLCVLMFIPESP 281  
Db 228 RARPLVMTLNSIG----FSFGHGLTAAVAYGVDTLTQLVSVPEFLCFIYSWMLAES 283  
QY 282 RWLISORPREADITIOKAKKN-----NTAVPAVIFDSVEELNPKQKAFITD 335  
Db 284 RWLITGRLDMLQELMKRYAPLNGKAVQDILTEPEVLLSARBELSMQGPASIGTILRM 343  
QY 336 RNIAITMTMSLLMLTSGVYFALSADAPNLHGDVYLNCFLSALIEIPAYITAMLLRTL 395  
Db 344 PGLRRRTCTISLWPAFFTEFGALDQALGNSIFLLQMFIGVYDIPAKMGALLLSHL 403  
QY 396 PRRTIIVAVLEWGGVLLFIQVLPDYFISIGLVMLGKREITAFPM 445  
Db 404 GRRLPLASLLLAGICLANTLVPEHMGALSALAVALGLGVGVAFCITITISSELEPTL 463  
QY 456 VNNMAVGTSTASRGTIAPFYVLYGAYNMLPYIWMGLTVLIGIF 503  
Db 464 LKMTAVGICQMAARAGAILGPLVRLLVGHGWPPLIYVGYTPVLSGLAALLPFTQSLPL 523  
QY 516 PETLEQMK 533  
Db 524 PDTIQDVQ 531

RESULT 8  
US-10-095-139-17  
Sequence 17, Application US/10095139  
Patent No. US20020165357A1  
GENERAL INFORMATION:



1 MRDYDEVIAFGWGPFORLIFLLSASIPNGNGM--SVJLAGTPEHRCRVPDAN 57

OY 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIPNGNGM---SVI<sup>1</sup>LAGTPEHRCRVPDAN 57

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Db      1 MEQEARVLAAGFGGARRL---LASAWPCIVLGLVLSSEELTAQAPAPICR--PDPTL 56
QY      58 LSSAMR-----NNSVP-----LRLDGHEVHSCSRYLATIANSSAG 96
Db      57 LPPALALAGPALLDAITPLGFTTRASPCLLRYPD-----PAPCTR----- 99
QY      97 LEPGRVDLGLQLEBOESCLDGEFSOD--VYLSVTVMNLVCEDNMKVPLTSLFVGV 154
Db      100 --PGRPAPARNGTCTCTGMLYALPGAGLQSPVQWMLVCGDGKVFLEQVSHLGL 157
QY      155 LGSFVSGQLSDRGKRNVLFAITAVQGSFLQISISWEMTVLFVIVMGQISNVYA 214
Db      158 LGCVILLGACDRGRRAVVASLVLTGTGASALASAPTLVITLILHG--GTIAGALLA 216
QY      215 FILG--TEILGKSVRIIFSTLGYCTFFAVGVMLPLFAFIRDMRL--LALVYPCVLCVP 272
Db      217 LYLARLECDPPRLRFS--MGAGLFESVGTLLPGLAALVQDMRLQGLGALMSGILL- 274
QY      273 LWMF---IPESPMLISORRFRREADIIOKAKMNTAVPAVIFDSVEELNPLKOOKA 329
Db      275 FMGFPAFPESPOMLATGQVARRKILMRFAASVD--DPLEENSLATELTML 330
QY      330 -----LDFRT-----RNIAIMTMSILLMMLTSVGYFALSIDAPMLHGDAYLN 373
Db      331 SARSPQRYHSPGLRTRVWTRNGLLTGFSSIVGGIRASFRSLAPQVPTF---YLP 386
QY      374 CELSALIEIPAYITAMLLRTLPRLR--YIIAAVLFWGCVLLFI---QLVP--VDIYFLSLG 428
Db      387 YFEAELEAAALVFLLTADCCGRRPVLGLTGWVGLASLLLAGAQLVGTWVLELV 445
QY      429 LVMLGFGITSAFSLVFTAEIPLTVLRNMAVGVTSTASRVGSIIAPFYVIGAVNRML 488
Db      446 ---LGLASRAVSALSLFAAEVFPVIRGAGGIVLGAGFLGAQAPLDITLGRGFFL 502
QY      489 PIYMGSLVYLIGITFLFEPESLGMTLPETLEOMOKV 526
Db      503 QQVVFASLAVLALLCVLLPESSRSRGLPOSTLODADRLR 540

```

## RESULT 13

```

US-09-738-626-6795
; Sequence 6795, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, MAKOTO
; APPLICANT: SENOH, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6795
; LENGTH: 448
; TYPE: PRN
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6795

```

```

Query Match      10.7%; Score 305.5; DB 9; Length 448;
Best Local Similarity 26.9%; Pred. No. 4.1e-18;
Matches 123; Conservative 62; Mismatches 190; Indels 83; Gaps 19;

QY      116 GMEF--SQDV-----YLSVTVMNLVCEDNMKVPLTSLF---FVGLLGSFVSGQLSD 165
Db      37  GWALDAMVGLISFVMAALATWML-----SPTEISLGSISFVGMALGASIGGLIAD 89
QY      166 RGRKRVNLFATM---AVQGSFLQISISWEMTVLFVIVMGQISNVYAFILGTEIL 222
Db      90  KLRGRQVRLSLIYGVATGASAL---SVSLAMLMALFEVGLGIGALPVASTLISEFS 146
QY      223 GKSVR-----IIFSTLGYCTFFAVGVMLPLFAFYI---RDMRLALATVPVGLCVPL 273
Db      147 PRKVRGRNVILE-----AFNALGIMAIYGTFFVAGSDGWRALALGCVPAIANYV 201
QY      274 WMFIDESPRLMISORRFRREADI---OKAKMNN---TAVPAVIFDSVEELNPLKOOKA 327
Db      202 RLGLPESVRFLEKKGRHDEAELIVSFEEAAAEKADATTAVVDHNAEGSVISWSAA 261
QY      328 FILDFFRRNIAIMTMSILLMMLTSVGYFALSIDAPL---HGDAYLNCFLSALI----- 380
Db      262 ---LRRRYALW---IWFCTINLSYGAFTWIPSLVADGFTLVKSFQPTLITTLA 311
QY      381 EIPAYITAMLLRTLPRLRYIIAAVLFWGCVLLFIQVVDYFSLIGLVMLGFGITSA 440
Db      312 QLPGYAVALAMLEKKGRSTLATPLVGSALSAALGLANVMQILVAGCLL--SFFNLGA 369
QY      441 FSLVFTAEIPLTVLRNMAVGVTSTASRVGSIIAPFYVIGAVNRMLPIYMGSLTVLI 500
Db      370 WQALYAIPELPTVNRGTGAAAGFRISAIIPLV-----PPVIAFGPIALF 421
QY      501 GFTLFPES--LGMTLPETLEOMOKVMPFSGKTRD 536
Db      422 ALFAFAIAIAIAFTLPE-----QKGSILAD 448

```

## RESULT 14

```

US-09-860-232A-7
; Sequence 7, Application US/09860232A
; Patent No. US2002028494A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A.J.
; TITLE OF INVENTION: 57256 AND 58289, NOVEL HUMAN
; TITLE OF INVENTION: TRANSPORTERS AND USES THEREOF
; FILE REFERENCE: 381552001500
; CURRENT APPLICATION NUMBER: US/09/860,232A
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,288
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 486
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-09-860-232A-7

```

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Query Match      9.8%; Score 280; DB 10; Length 486;
Best Local Similarity 26.1%; Pred. No. 7e-16;
Matches 119; Conservative 78; Mismatches 179; Indels 80; Gaps 15;

QY      126 STVVTVMNLVCEDNMKVPLTSLFVGVLLGSFVSGQLSDRFRGRN-----VLFATMAV 179
Db      48  SYVLF-----GLVYSIFRIGRLISLFGKRGDRGKRKSLILALVFLVICAL 95
QY      180 QRGFS--FLQFISISWEMTVLFVIVMGQISNVYAAIITELIGKSVR-----IIF 230
Db      96  LGAAPAGYTTIGLMAFYLITVGRVAVLGAGVASLYVMYISLAPKRLGALSGLYOLA 155
QY      231 STLGVCTFEFAVGYMLPL---FAVFIRDMRLALATVPVGLVCPIMWFIDESPRLISQ 287

```

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Db 156 ITGIIIVAAIIGLGNKTNDSALNSGWRIPGLQVLPALLLIGLLEPESRMLVER 215
QY 288 RRFREARDIIQKAKAMNT-----AYPAVFDSVEELNPLKOOKATLDFRR---NTA 339
Db 216 GKLEAEAEVAKLRGVEDVDIOEIKAELEAVEE---EKAKAWGELFRKTRPKPR 272
QY 340 IMTMSLLMLTSGVFALSLDAPNLH-----GDAYLNCFLSALLEIPAYITAMLLRT 394
Db 273 QRLMGVLOPQOLTGINAFYYSPITFKSVGSDBASLLVYIIGVAVNEFTVALLAF 332
QY 395 LPRRYIAAVLEWGG-----GVLLFIQVDPVYFISIGLMLKFGSITSA 440
Db 333 LVDFGRRLILLGAAGMAICFLLIGASIGVALLLNKPKDPLSKAGIYAVIFILLFIA 392
QY 441 FSNL-----YVFTAEIYPTLVNMAVGVTASRVSIIA---PYF-----VYLGAVN 485
Db 393 FFLGCGPIPWILSELFPYKRSKALALATANMLANFLIGFLFPYITGALGLAGY- 451
QY 486 RMLPYVMGSLTVLIGIFTLF--PESIGMTLPETLE 520
Db 452 ---VFLVFAGLVLFLFVFFVETKGRLEIEE 484
```

```
RESULT 15
US-10-170-528-5
; Sequence 5, Application US/10170528
; Publication No. US20030009024A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 46384, A Human Transporter Family Member
; FILE REFERENCE: MPI01-092PIRM
; CURRENT APPLICATION NUMBER: US/10/170,528
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/298,012
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for PFAM PF00083
US-10-170-528-5
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Query Match 9.7%; Score 276.5; DB 9; Length 488;  
Best Local Similarity 25.2%; Pred. No. 1.4e-15;  
Matches 129; Conservative 83; Mismatches 186; Indels 113; Gaps 20;

```
QY 84 YRIATTANFSALGLEPGRDVD---LGLEQESCLDGEFSODVYLTVTENLVCEDN 139
Db 15 YDTGVIGGFLAL-----IDFLFRGLLTSSGAL-----AELVGYSTVLT----- 53
QY 140 WKVPLTTSLEFVGVVLGFSYSGOLSDRFGRKN-----VLPATMAVQTGS--FLQIFSI 191
Db 54 ---GLVVSIFELRLGLSLFAGKIGDRFGSKSLIALVLFVIGALLSGAAPGYTTIGLM 110
QY 192 SWEMFVLYFIYVGMQISNVVAFILGTTELIGKSVR-----IIFSTIGVCTFFAVGYM 244
Db 111 AFYLLLVGRVLVGLVGASVLPMTISEAPKALRGALGSYQLAITTIGILVAATIGLG 170
QY 245 LRLP---FAFFIDRMMLLIALTPGVLCPPLMWFIPESRMLISORRFREADIIOKAA 301
Db 171 LKTNDSALNSGWRIPGLQVLPALLLIGLLEPESRMLVEKGRLEAEAREVL---A 227
QY 302 KANNTAVPAVIFSVDELNPLKQO-----KATLDFR-----TRNIAIMTIA 344
Db 228 KLGK-----VEDVDIOEIKAELEATVSEERKAGKSWGELFRGTRPKVRQRLMGYV 281
QY 345 SLLMLTSGVFALSLDAPNLH-----GDAYLNCFLSALLEIPAYITAMLLRTLPY 399
```

```
Db 282 IQAFOOLGIN--AIFYSPITFKSVGSVASLLTVIIGVAVNEFTVALLFIYDRF 339
QY 400 IIAAVLFWGG-----GVLLFIQVDPVYFISIGLMLKFGSITSAFSL- 444
Db 340 GRRPILLIGAAGMAICFLLIGASIGVALLLNKPKDPSKAGIYAVIFILLFIAFPALG 399
QY 445 ---YVFTAEIYPTLVNMAVGVTASRVSIIA---PYF-----VYLGAVNRLMPY 490
Db 400 WGPPIWVILSELFPYKRSKALALATANMLANFLIGFLFPYITGALGLAGY-----VF 455
QY 491 IVMGSLTVLIGIFTLF--PESIGMTLPETLE 520
Db 456 LVFAGLVLFLFVFFVETKGRLEIEE 486
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Search completed: July 3, 2003, 12:43:09  
Job time : 27 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2003, 12:35:54 ; Search time 51 Seconds

(without alignments)  
2818.424 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845

Sequence: 1 MRDYDEVIAFLGEMGPFORL.....KTRDSMETEENPKVLTAF 551

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1203519 seqs, 260870444 residues

Total number of hits satisfying chosen parameters: 1203519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep4:\*  
2: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep4:\*  
3: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep4:\*  
4: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep4:\*  
5: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep4:\*  
6: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep4:\*  
7: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep4:\*  
8: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep4:\*  
9: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep4:\*  
10: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep4:\*  
11: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep4:\*  
12: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep4:\*  
13: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep4:\*  
14: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID                  | Description        |
|------------|--------|-------------|--------|---------------------|--------------------|
| 1          | 2845   | 100.0       | 551    | US-10-327-189-7     | Sequence 7, Appl   |
| 2          | 2839   | 99.8        | 551    | US-10-327-189-38    | Sequence 38, Appl  |
| 3          | 2833   | 99.6        | 551    | US-10-327-189-2     | Sequence 2, Appl   |
| 4          | 2218   | 78.0        | 557    | US-09-949-016-6309  | Sequence 6309, Ap  |
| 5          | 2218   | 78.0        | 557    | US-10-327-189-4     | Sequence 4, Appl   |
| 6          | 2166   | 76.1        | 551    | US-60-453-135-12520 | Sequence 12520, A  |
| 7          | 2166   | 76.1        | 551    | US-60-453-050-12520 | Sequence 12520, A  |
| 8          | 2166   | 76.1        | 551    | US-60-466-412-12520 | Sequence 12520, A  |
| 9          | 2166   | 76.1        | 551    | US-09-949-016-7929  | Sequence 7929, Ap  |
| 10         | 2034.5 | 71.5        | 564    | US-10-326-820-2     | Sequence 2, Appl   |
| 11         | 1445   | 50.8        | 304    | US-09-724-676-96956 | Sequence 96956, A  |
| 12         | 1445   | 50.8        | 304    | US-09-724-676-96956 | Sequence 96956, A  |
| 13         | 794.5  | 27.9        | 577    | US-10-038-854-163   | Sequence 163, App  |
| 14         | 779.5  | 27.4        | 560    | US-10-218-140-5604  | Sequence 5604, App |
| 15         | 740.5  | 25.0        | 534    | US-10-038-854-28    | Sequence 28, Appl  |
| 16         | 714.5  | 25.1        | 526    | US-10-038-854-30    | Sequence 30, Appl  |
| 17         | 704    | 24.7        | 555    | US-60-453-135-13981 | Sequence 13981, A  |
| 18         | 704    | 24.7        | 555    | US-60-453-135-13981 | Sequence 13981, A  |
| 19         | 704    | 24.7        | 555    | US-60-453-050-13981 | Sequence 13981, A  |

|    |       |      |     |                      |                   |
|----|-------|------|-----|----------------------|-------------------|
| 20 | 704   | 24.7 | 555 | US-60-466-412-13981  | Sequence 13981, A |
| 21 | 703   | 24.7 | 555 | PCT-US02-29560-248   | Sequence 248, App |
| 22 | 703   | 24.7 | 555 | PCT-US02-19592-104   | Sequence 104, App |
| 23 | 703   | 24.7 | 555 | US-10-245-882-248    | Sequence 248, App |
| 24 | 703   | 24.7 | 555 | US-10-295-027-300    | Sequence 300, App |
| 25 | 690.5 | 24.3 | 419 | US-10-038-854-371    | Sequence 371, App |
| 26 | 685.5 | 24.1 | 554 | US-60-453-135-9175   | Sequence 9175, Ap |
| 27 | 685.5 | 24.1 | 554 | US-60-453-050-9175   | Sequence 9175, Ap |
| 28 | 685.5 | 24.1 | 554 | US-60-466-412-9175   | Sequence 9175, Ap |
| 29 | 673   | 23.7 | 535 | US-10-219-051B-3126  | Sequence 3126, Ap |
| 30 | 673   | 23.7 | 535 | US-10-219-051B-3130  | Sequence 3130, Ap |
| 31 | 673   | 23.7 | 535 | US-10-219-051B-12729 | Sequence 12729, A |
| 32 | 673   | 23.7 | 535 | US-10-219-051B-12733 | Sequence 12733, A |
| 33 | 671   | 23.6 | 556 | US-09-949-016-7027   | Sequence 7027, Ap |
| 34 | 671   | 23.6 | 556 | US-60-422-176-49     | Sequence 49, Appl |
| 35 | 671   | 23.6 | 556 | US-60-453-135-13982  | Sequence 13982, A |
| 36 | 671   | 23.6 | 556 | US-60-453-050-13982  | Sequence 13982, A |
| 37 | 671   | 23.6 | 556 | US-60-466-412-13982  | Sequence 13982, A |
| 38 | 671   | 23.6 | 556 | US-09-949-016-10036  | Sequence 10036, A |
| 39 | 654   | 23.0 | 547 | US-09-949-016-7043   | Sequence 7043, Ap |
| 40 | 654   | 23.0 | 547 | US-60-452-680-18592  | Sequence 18592, A |
| 41 | 653.5 | 23.0 | 456 | US-10-038-854-164    | Sequence 164, App |
| 42 | 653.5 | 23.0 | 548 | US-10-219-051B-3128  | Sequence 3128, Ap |
| 43 | 653.5 | 23.0 | 548 | US-10-219-051B-3132  | Sequence 3132, Ap |
| 44 | 653.5 | 23.0 | 548 | US-10-219-051B-12731 | Sequence 12731, A |
| 45 | 653.5 | 23.0 | 548 | US-10-219-051B-12735 | Sequence 12735, A |

## ALIGNMENTS

RESULT 1  
US-10-327-189-7  
Sequence 7, Application US/10327189  
GENERAL INFORMATION:  
APPLICANT: Peltekova, Yanya D  
APPLICANT: Wintle, Richard F  
APPLICANT: Rudin, Laurence A  
APPLICANT: Peter, St George-Hyslop H  
APPLICANT: Siminovich, Katherine A  
TITLE OF INVENTION: POLYMORPHISMS OF THE OCTIN1 AND OCTIN2 CATION TRANSPORTERS ASSOC  
FILE REFERENCE: ELLP-020  
CURRENT APPLICATION NUMBER: US/10/327,189  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: 60/362,700  
PRIOR FILING DATE: 2002-03-08  
PRIOR APPLICATION NUMBER: 60/343,338  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: 60/427,529  
PRIOR FILING DATE: 2002-11-19  
PRIOR APPLICATION NUMBER: 60/362,717  
PRIOR FILING DATE: 2002-03-08  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 551  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-327-189-7  
Query Match 100.0%; Score 2845; DB 12; length 551;  
Best Local Similarity 100.0%; Pred. No. 3.5e-250;  
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRDYDEVIAFLGEMGPFORLIFFLSASITPNFGNGSVYFLAGTPEHRCRPDAANLSS 60  
DB 1 MRDYDEVIAFLGEMGPFORLIFFLSASITPNFGNGSVYFLAGTPEHRCRPDAANLSS 60  
QY 61 AMRNNVPLRLRGREVPSCSRRLATTANFSALEPGRDVDLGLDQESCLDQWERS 120  
DB 61 AMRNNVPLRLRGREVPSCSRRLATTANFSALEPGRDVDLGLDQESCLDQWERS 120

QY 121 QDYLSTVTEWNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180  
DB 121 QDYLSTVTEWNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180  
QY 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEA 240  
DB 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEA 240  
QY 241 VGYMLPLFAVFIKDMRMLLALVPGVLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
DB 241 VGYMLPLFAVFIKDMRMLLALVPGVLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
QY 301 AKANNVAVPAVIFDSVEELNPKQOKAFILDFRTNIAIMTISLLMMLTSVGFALS 360  
DB 301 AKANNVAVPAVIFDSVEELNPKQOKAFILDFRTNIAIMTISLLMMLTSVGFALS 360  
QY 361 LDAPNLHGDVYLNCFSLALIEIPAYITMMLLRTLPRTYITAAVLPFGGVLFIQVLPV 420  
DB 361 LDAPNLHGDVYLNCFSLALIEIPAYITMMLLRTLPRTYITAAVLPFGGVLFIQVLPV 420  
QY 421 DYFFLSIGVLMGKFGITSASFMLVFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
DB 421 DYFFLSIGVLMGKFGITSASFMLVFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
QY 481 LGAVNRMLPYIVMGSILVLIIGITLFPESLGMTPETLEOMQKVMFRSGKTRDSMET 540  
DB 481 LGAVNRMLPYIVMGSILVLIIGITLFPESLGMTPETLEOMQKVMFRSGKTRDSMET 540  
QY 541 EENPKVLITAF 551  
DB 541 EENPKVLITAF 551

## RESULT 2

US-10-327-189-38  
; Sequence 38, Application US/10327189  
; GENERAL INFORMATION:  
; APPLICANT: Peltekova, Yanya D  
; APPLICANT: Wintle, Richard F  
; APPLICANT: Rubin, Laurence A  
; APPLICANT: Peter, St George-Hyslop H  
; APPLICANT: Simnovitch, Katherine A  
; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIAT  
; TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS  
; FILE REFERENCE: ELP-020  
; CURRENT APPLICATION NUMBER: US/10/327,189  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 60/362,700  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/343,338  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/427,529  
; PRIOR FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/362,717  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 551  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-327-189-38

Query Match 99.8%; Score 2839; DB 12; Length 551;  
Best Local Similarity 99.8%; Pred. No. 1.2e-249;  
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MRDYDEVIAFLGEMGFORLIFELLASITIPNGFNMSVYVLAGTPEHRCVPPDANLSS 60  
DB 1 MRDYDEVIAFLGEMGFORLIFELLASITIPNGFNMSVYVLAGTPEHRCVPPDANLSS 60  
QY 61 AMRNSVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVDLQLEQESCLDGMES 120  
DB 61 AMRNSVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVDLQLEQESCLDGMES 120

DB 61 AMRNSVPLRLRDGREVPHSCSRYLATIANFSALGLEPGRDVDLQLEQESCLDGMES 120  
QY 121 QDYLSTVTEWNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180  
DB 121 QDYLSTVTEWNLVCEDNKKVPLTSLFVGVLLGSFVSGQLSDRFGRKNVLPATMAVQ 180  
QY 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEA 240  
DB 181 TGFSFLOIFSIEMEFVLFVYVGMGOISNYVAFLIGTEILGKSVRIIFSTLGVCTFEA 240  
QY 241 VGYMLPLFAVFIKDMRMLLALVPGVLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
DB 241 VGYMLPLFAVFIKDMRMLLALVPGVLCVPLMWFIPESPRMLISORREAEEDIIOKA 300  
QY 301 AKANNVAVPAVIFDSVEELNPKQOKAFILDFRTNIAIMTISLLMMLTSVGFALS 360  
DB 301 AKANNVAVPAVIFDSVEELNPKQOKAFILDFRTNIAIMTISLLMMLTSVGFALS 360  
QY 361 LDAPNLHGDVYLNCFSLALIEIPAYITMMLLRTLPRTYITAAVLPFGGVLFIQVLPV 420  
DB 361 LDAPNLHGDVYLNCFSLALIEIPAYITMMLLRTLPRTYITAAVLPFGGVLFIQVLPV 420  
QY 421 DYFFLSIGVLMGKFGITSASFMLVFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
DB 421 DYFFLSIGVLMGKFGITSASFMLVFTAEPLTVRNMAVGVSTASRVGSIAPYFY 480  
QY 481 LGAVNRMLPYIVMGSILVLIIGITLFPESLGMTPETLEOMQKVMFRSGKTRDSMET 540  
DB 481 LGAVNRMLPYIVMGSILVLIIGITLFPESLGMTPETLEOMQKVMFRSGKTRDSMET 540  
QY 541 EENPKVLITAF 551  
DB 541 EENPKVLITAF 551

## RESULT 3

US-10-327-189-2  
; Sequence 2, Application US/10327189  
; GENERAL INFORMATION:  
; APPLICANT: Peltekova, Yanya D  
; APPLICANT: Wintle, Richard F  
; APPLICANT: Rubin, Laurence A  
; APPLICANT: Peter, St George-Hyslop H  
; APPLICANT: Simnovitch, Katherine A  
; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOC  
; TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS  
; FILE REFERENCE: ELP-020  
; CURRENT APPLICATION NUMBER: US/10/327,189  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 60/362,700  
; PRIOR FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/343,338  
; PRIOR FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/427,529  
; PRIOR FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/362,717  
; PRIOR FILING DATE: 2002-03-08  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 551  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-10-327-189-2

Query Match 99.6%; Score 2833; DB 12; Length 551;  
Best Local Similarity 99.6%; Pred. No. 4.4e-249;  
Matches 549; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MRDYDEVIAFLGEMGFORLIFELLASITIPNGFNMSVYVLAGTPEHRCVPPDANLSS 60  
DB 1 MRDYDEVIAFLGEMGFORLIFELLASITIPNGFNMSVYVLAGTPEHRCVPPDANLSS 60



```
Db 61 AMRNHTVPLRLDRGREVPHSCRRYRLATTIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
QY 121 ODVYLSVTYEMNLVCEDMNKVPLTSLFVGVLLSFGVSGOLSDRGKRVNLFATMAVO 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ODVYLSVTYEMNLVCEDMNKVPLTSLFVGVLLSFGVSGOLSDRGKRVNLFATMAVO 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 TGFSEFLOIFSISWEMFVLFVYVGMGOISNVVAFLIGTEILGKSVRIIFSTLGVCTFEA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 TGFSEFLOIFSISWEMFVLFVYVGMGOISNVVAFLIGTEILGKSVRIIFSTLGVCTFEA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VGYMLPLFAFIRDMRMMLLALTVPVGLVPLMTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VGYMLPLFAFIRDMRMMLLALTVPVGLVPLMTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AKANNTAVPAVIFD--SVEELNPLKQOKAFILDLFRTNIAIMTISLMLMTISGYFA 358
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 AKANGIYVPSITFDPSLODLSKSKQOSHILDLRTNIRMTYIMSLMTISGYGFG 360
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRLTPRYIIAVALFWGGVLLFIOLV 418
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAAMLLOLPRRYSMATLFLGGSVLLFMOLV 420
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 PVDYFELSLGVMLGKPGITSAFSLMVFYTAELPVTYRNMAVGTASVSGSIAPYE 478
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 PPDLYLATVLMVWGKFEVTAFAFSNVYTAELPVTYRNMGVSSASTASRLGSIISPYE 480
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 VYLGAYNRMPLPYIVMGSILVLIIGITLFFPESLSGMLTPETLEQOMQKWFPSGK---KTR 535
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 VYLGAYDRFLPYIIMGSLTILTLTLFLPESGTPLPPTIDOMLRYKMKHRTTPSHR 540
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 536 DSMETEENPKVL-ITAF 551
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 MKDQGERPTILKSTAF 557
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
US-60-453-135-12520
; Sequence 12520, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olgia
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12520
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-12520
```

```
Query Match 76.1%; Score 2166; DB 14; Length 551;
Best Local Similarity 74.9%; Pred. No. 2.3e-188;
Matches 417; Conservative 57; Mismatches 71; Indels 12; Gaps 4;
```

```
QY 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFGMSVFLAGTPHRCRVDPANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFGMSVFLAGTPHRCRVDPANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AMRNNSVPLRLDRGREVPHSCRRYRLATTIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AMRNHTVPLRLDRGREVPHSCRRYRLATTIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 ODVYLSVTYEMNLVCEDMNKVPLTSLFVGVLLSFGVSGOLSDRGKRVNLFATMAVO 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ODVYLSVTYEMNLVCEDMNKVPLTSLFVGVLLSFGVSGOLSDRGKRVNLFATMAVO 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 TGFSEFLOIFSISWEMFVLFVYVGMGOISNVVAFLIGTEILGKSVRIIFSTLGVCTFEA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 TGFSEFLOIFSISWEMFVLFVYVGMGOISNVVAFLIGTEILGKSVRIIFSTLGVCTFEA 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
QY 241 VGYMLPLFAFIRDMRMMLLALTVPVGLVPLMTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 FGIVMLPLFAFIRDMRMMLLALTVPVGLVPLMTIPESPRMLISQRREREADIIQKA 294
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AKANNTAVPAVIFD--SVEELNPLKQOKAFILDLFRTNIAIMTISLMLMTISGYFA 358
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 AKANGIYVPSITFDPSLODLSKSKQOSHILDLRTNIRMTYIMSLMTISGYGFG 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 LSLDAPNLHGDAYLNCFLSALIEIPAYITAMLLRLTPRYIIAVALFWGGVLLFIOLV 418
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 355 LSLDTPNLHGDIFVNCFLSAMVEVPAYVLAAMLLOLPRRYSMATLFLGGSVLLFMOLV 414
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 PVDYFELSLGVMLGKPGITSAFSLMVFYTAELPVTYRNMAVGTASVSGSIAPYE 478
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 415 PPDLYLATVLMVWGKFEVTAFAFSNVYTAELPVTYRNMGVSSASTASRLGSIISPYE 474
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 VYLGAYNRMPLPYIVMGSILVLIIGITLFFPESLSGMLTPETLEQOMQKWFPSGK---KTR 535
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 475 VYLGAYDRFLPYIIMGSLTILTLTLFLPESGTPLPPTIDOMLRYKMKHRTTPSHR 534
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 536 DSMETEENPKVL-ITAF 551
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 535 MKDQGERPTILKSTAF 551
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 7
US-60-453-050-12520
; Sequence 12520, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: LUKE, May
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12520
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-12520
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Query Match 76.1%; Score 2166; DB 14; Length 551;
Best Local Similarity 74.9%; Pred. No. 2.3e-188;
Matches 417; Conservative 57; Mismatches 71; Indels 12; Gaps 4;
```

```
QY 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFGMSVFLAGTPHRCRVDPANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRDYDEVIAFLGEMGPFQRLIFLLSASIIIPNGFGMSVFLAGTPHRCRVDPANLSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 AMRNNSVPLRLDRGREVPHSCRRYRLATTIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 AMRNHTVPLRLDRGREVPHSCRRYRLATTIANFSALGLEPGRDVLGQLEQESCLDGEFS 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 ODVYLSVTYEMNLVCEDMNKVPLTSLFVGVLLSFGVSGOLSDRGKRVNLFATMAVO 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ODVYLSVTYEMNLVCEDMNKVPLTSLFVGVLLSFGVSGOLSDRGKRVNLFATMAVO 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 TGFSEFLOIFSISWEMFVLFVYVGMGOISNVVAFLIGTEILGKSVRIIFSTLGVCTFEA 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 175 TGFSEFLOIFSISWEMFVLFVYVGMGOISNVVAFLIGTEILGKSVRIIFSTLGVCTFEA 234
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 VGYMLPLFAFIRDMRMMLLALTVPVGLVPLMTIPESPRMLISQRREREADIIQKA 300
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 FGIVMLPLFAFIRDMRMMLLALTVPVGLVPLMTIPESPRMLISQRREREADIIQKA 294
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 AKANNTAVPAVIFD--SVEELNPLKQOKAFILDLFRTNIAIMTISLMLMTISGYFA 358
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 295 AKANGIYVPSITFDPSLODLSKSKQOSHILDLRTNIRMTYIMSLMTISGYGFG 354
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```



Db 594 MKDQGERPTILKSTAR 610

RESULT 10  
US-10-326-820-2  
Sequence 2, Application US/10326820  
GENERAL INFORMATION:  
APPLICANT: Thadd C. Reeder  
TITLE OF INVENTION: Organic Cation Transporter (OCTN3)  
TITLE OF INVENTION: Disruptions, Compositions and Methods Relating Thereto  
FILE REFERENCE: R-1493  
CURRENT APPLICATION NUMBER: US/10/326,820  
CURRENT FILING DATE: 2002-12-20  
PRIOR APPLICATION NUMBER: US 60/342,490  
PRIOR FILING DATE: 2001-12-21  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FASTEST for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 564  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
OTHER INFORMATION: Targeting Vector  
US-10-326-820-2

Query Match  
Best Local Similarity 71.5%; Score 2034.5; DB 12; Length 564;  
Matches 380; Conservative 75; Mismatches 85; Indels 11; Gaps 3;

QY 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVDPANLSS 60  
Db 1 MLDYEVIAFLGEMGFQRLIFLLSASIIIPNGFTGLSAFLAIEHRCRIPDVNLSS 60  
QY 61 AMRNNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVLGQLEQESCLDGEWFS 120  
Db 61 AMRNNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVLGQLEQESCLDGEWFS 120  
QY 121 ODVYLSVVTENMLVCEENMKVPLTSLTFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
Db 121 KOFLSLTIVTEMLVCEENMKVPLTSLTFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
QY 181 TGFSFLQIFSISMEFTVLFVYVGMQISNRYVAFILGTETLIGSVRIIFSTLGVCTEFA 240  
Db 181 TGFSFLQIFSISMEFTVLFVYVGMQISNRYVAFILGTETLIGSVRIIFSTLGVCTEFA 240  
QY 241 VGYMLPLFAVFIKDRMMLLATLVPGVLCVPLMFIIPSPRLISQGRKKEVEVITRA 300  
Db 241 FGEVVLPLFAVFIKDRMMLLATLVPGVLCVPLMFIIPSPRLISQGRKKEVEVITRA 300  
QY 301 AKMNNMTAVPAVIDSVSEELNPL-----KQKAFIIDLFTRNAIATMTISLLMMLTSV 354  
Db 301 AKINGIAPSTIFDP-SETKKLQDDSSKKPKQSHIYIDVTRPIRILTIMSIIMLTISV 359  
QY 355 GYFALSIDAPNLHGDAYLNCFLSALTEIPAYITAMLLTLPRIYIAAVLEWGGVLLF 414  
Db 355 GYFALSIDAPNLHGDAYLNCFLSALTEIPAYITAMLLTLPRIYIAAVLEWGGVLLF 414  
QY 415 IOAVPYDYPLSTIGVLMGKFGTISAFSMUYVFTATPLVIRNNMVGVTASIRGSTII 474  
Db 420 VOLVPSDLATLSTLTMVGKFGTISASVNYVYTAELIPLVANNMGVGSSTASIRGSTII 479  
QY 475 APFYVYLGAAYNRMLPYIVMGSLLVLIGIFLTFEPESIGMTLPETLEQOMKRVWFRSGKKT 534  
Db 480 SPFYVYLGAAYNRMLPYIVMGSLLVLIGIFLTFEPESIGMTLPETLEQOMKRVWFRSGKKT 534  
QY 535 RDSMEIEENPK 545  
Db 536 RSLSKRGSPK 546

RESULT 11  
US-09-724-676-96956

Sequence 96956, Application US/09724676  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676  
CURRENT FILING DATE: 2000-11-28  
NUMBER OF SEQ ID NOS: 97222  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 96956  
LENGTH: 304  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676-96956

Query Match  
Best Local Similarity 50.8%; Score 1445; DB 10; Length 304;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVDPANLSS 60  
Db 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVDPANLSS 60  
QY 61 AMRNNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVLGQLEQESCLDGEWFS 120  
Db 61 AMRNNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVLGQLEQESCLDGEWFS 120  
QY 121 ODVYLSVVTENMLVCEENMKVPLTSLTFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
Db 121 ODVYLSVVTENMLVCEENMKVPLTSLTFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
QY 181 TGFSFLQIFSISMEFTVLFVYVGMQISNRYVAFILGTETLIGSVRIIFSTLGVCTEFA 240  
Db 181 TGFSFLQIFSISMEFTVLFVYVGMQISNRYVAFILGTETLIGSVRIIFSTLGVCTEFA 240  
QY 241 VGYMLPLFAVFIKDRMMLLATLVPGVLCVPLMFIIPSPRLISQGRKKEVEVITRA 300  
Db 241 VGYMLPLFAVFIKDRMMLLATLVPGVLCVPLMFIIPSPRLISQGRKKEVEVITRA 300

RESULT 12  
US-09-724-676a-96956  
Sequence 96956, Application US/09724676a  
GENERAL INFORMATION:  
APPLICANT: Compugen LTD  
TITLE OF INVENTION: Variants of alternative splicing  
FILE REFERENCE: 129181.4 Compugen  
CURRENT APPLICATION NUMBER: US/09/724,676a  
CURRENT FILING DATE: 2000-11-28  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 96956  
LENGTH: 304  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-724-676a-96956

Query Match  
Best Local Similarity 50.8%; Score 1445; DB 10; Length 304;  
Matches 275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVDPANLSS 60  
Db 1 MRDYEVIAFLGEMGFQRLIFLLSASIIIPNGFNGMSVFLAGTPHRCRVDPANLSS 60  
QY 61 AMRNNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVLGQLEQESCLDGEWFS 120  
Db 61 AMRNNSVPLRLDGRVPHSCSRVRLATIANFSALGLEPGRDVLGQLEQESCLDGEWFS 120  
QY 121 ODVYLSVVTENMLVCEENMKVPLTSLTFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180  
Db 121 ODVYLSVVTENMLVCEENMKVPLTSLTFVGVLLGSFVSGQLSDRGKRVLPATMAVQ 180

OY 181 TGFSFLOIFSIWMEFTLVFYVGMQISNVVAFILGTETILGKSVRIIFSTLGVCTFFA 240  
 Db 181 TGFSFLOIFSIWMEFTLVFYVGMQISNVVAFILGTETILGKSVRIIFSTLGVCTFFA 240  
 OY 241 VGYMLLPFAFIFIRDMRMLLALTVPGVLCVPLMW 275  
 Db 241 VGYMLLPFAFIFIRDMRMLLALTVPGVLCVPLMW 275

## RESULT 13

US-10-038-854-163  
 ; Sequence 163, Application US/10038854  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Spytek, Kimberly A  
 ; APPLICANT: Li, Li  
 ; APPLICANT: Wolenc, Adam R  
 ; APPLICANT: Vernet, Corine  
 ; APPLICANT: Eisen, Andrew J  
 ; APPLICANT: Liu, Xiaohong  
 ; APPLICANT: Malyankar, Uriel M  
 ; APPLICANT: Shimkets, Richard A  
 ; APPLICANT: Tcherenev, Vellizar  
 ; APPLICANT: Spaderna, Steven K  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Kekuda, Ramesh  
 ; APPLICANT: Paturajan, Meera  
 ; APPLICANT: Gusev, Vladimir Y  
 ; APPLICANT: Gangolli, Esha A  
 ; APPLICANT: Guo, Xiaojia S  
 ; APPLICANT: Shenoy, Suresh G  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Caeman, Stacie J  
 ; APPLICANT: Boldog, Ferenc  
 ; APPLICANT: Burgess, Catherine E  
 ; APPLICANT: Edinger, Shlomit R  
 ; APPLICANT: Ellerman, Karen  
 ; APPLICANT: Gunther, Erik  
 ; APPLICANT: Smithson, Glenda  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Macdougall, John R  
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
 ; FILE REFERENCE: 21402-230  
 ; CURRENT APPLICATION NUMBER: US/10/038,854  
 ; CURRENT FILING DATE: 2003-01-22  
 ; PRIOR APPLICATION NUMBER: 60/258,928  
 ; PRIOR FILING DATE: 2000-12-29  
 ; PRIOR APPLICATION NUMBER: 60/259,415  
 ; PRIOR FILING DATE: 2001-01-02  
 ; PRIOR APPLICATION NUMBER: 60/259,785  
 ; PRIOR FILING DATE: 2001-01-04  
 ; PRIOR APPLICATION NUMBER: 60/269,814  
 ; PRIOR FILING DATE: 2001-02-20  
 ; PRIOR APPLICATION NUMBER: 60/279,832  
 ; PRIOR FILING DATE: 2001-03-29  
 ; PRIOR APPLICATION NUMBER: 60/279,833  
 ; PRIOR FILING DATE: 2001-03-29  
 ; PRIOR APPLICATION NUMBER: 60/279,863  
 ; PRIOR FILING DATE: 2001-03-29  
 ; PRIOR APPLICATION NUMBER: 60/283,889  
 ; PRIOR FILING DATE: 2001-04-13  
 ; PRIOR APPLICATION NUMBER: 60/284,447  
 ; PRIOR FILING DATE: 2001-04-18  
 ; PRIOR APPLICATION NUMBER: 60/286,683  
 ; PRIOR FILING DATE: 2001-04-25  
 ; Remaining Prior Application data removed - See file wrapper or PAM.  
 ; NUMBER OF SEQ ID NOS: 411  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 163  
 ; LENGTH: 577  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-038-854-163

Query Match 27.9%; Score 794.5; DB 12; Length 577;  
 Best Local Similarity 32.5%; Pred. No. 1,86-63;  
 Matches 187; Conservative 117; Mismatches 222; Indels 49; Gaps 9;

OY 2 RDYDEVIAFLGEMGFQRLIFFLSASIIIPNGFNGSVYFLAGTEPHRCRV-----53  
 Db 4 RHEGEGYDVHGFGRGRQRLYFICAFQNSCIIHLASVEMKVTTHHCRRPGNNSQYVF 63  
 OY 54 -----DAANLSAMRNNSVPLRLRDGREVPS-CSSRLATIANFSAIGLEPGADV 103  
 Db 64 HNSHNSLDEDTGALLSSGQKDYVVOLONGEITMELSRCSRNKR---EWTSSIGYE-----115  
 OY 104 DLGQLEOESCLDGMESODVYLTSTVTEKNVYCEONMVPPLTSLFPGVLLGSVSGOL 163  
 Db 116 YTGSKKEPFCVGDYITDONTMKTSTAVTQNLVCDKRMAMLIQPLFMFGVLLGSVYGF 175  
 OY 164 SDFGRKRVLFATMAVQTGFSEFLQIFSIWMEFTLVFYVGMQISNVVAFILGTETILG 223  
 Db 176 SDRIGRRVYLMATSSMFLGIAAFVADYTFMARPFANVAGVLYVGVYMEFIG 235  
 OY 224 KSVRIIFSTLGYCTFFAVGYMLLPFAFIRDM---RMILLALTVPGVLCVPLMWFPDS 280  
 Db 236 MKSR-TWASVHLHSFPAVGTLLVLTGLVTRTMWLYOMLITSTVPFLICC---WVLPET 291  
 OY 281 PMLISORPREAEDITOKAKMNNTA-----VPAVIFDSVEELNPKQKAFLLDFR 334  
 Db 292 PFWLSEGRYERQKIVDIMAKMNRASSCKLSELLSLDQGVNSPFEVQKHNLSYLFY 351  
 OY 335 TRNIAIMTMSLLMMLTSVGFALSLDAPNLHGDAVINCPLSALIEIPAYITAMLLRT 394  
 Db 352 NMSIFKRTLVLWLMFTGSLGYFSINSVNLGNBEYINTLFLGVEIPAYIFVCIADK 411  
 OY 395 LPRRYIIANVLWGGVLLFQIOLVPDYDYFLSLGIVMGKFGITSAFSLVYFAELPYT 454  
 Db 412 VGRRTVLAISLCSALACGVAVVYIPQKHILGVVAVMGKFAIGAFILYLTALPYT 471  
 OY 455 LVNNMAVGTSTASRGSTIAPYFYLGVNMLYIYVWGSTLVIGLTFEPESLMT 514  
 Db 472 IYRSLAVGSGSNVCRSLASLAFPSVDSLSTWIFQIOLVGVALLSGVTLKLPETLGR 531  
 OY 515 LPETLEQMKVRWFRSGKTRDSMETENPKVLT 549  
 Db 532 LATWEAAKL-----ESENESKSKLLT 556

## RESULT 14

US-10-218-140-5604  
 ; Sequence 5604, Application US/10218140  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Leach, Martin D.  
 ; APPLICANT: Shimkets, Richard A.  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES  
 ; FILE REFERENCE: 15966-543 CON  
 ; CURRENT APPLICATION NUMBER: US/10/218,140  
 ; CURRENT FILING DATE: 2002-08-12  
 ; PRIOR APPLICATION NUMBER: 09/540,763  
 ; PRIOR FILING DATE: 2000-03-30  
 ; PRIOR APPLICATION NUMBER: 60/127,728  
 ; PRIOR FILING DATE: 1999-04-05  
 ; PRIOR APPLICATION NUMBER: 60/127,636  
 ; PRIOR FILING DATE: 1999-04-02  
 ; PRIOR APPLICATION NUMBER: 60/127,607  
 ; PRIOR FILING DATE: 1999-03-31  
 ; NUMBER OF SEQ ID NOS: 6322  
 ; SOFTWARE: Curator Version 1.0  
 ; SEQ ID NO 5604  
 ; LENGTH: 560  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-218-140-5604

Query Match

27.4%; Score 779.5; DB 12; Length 560;



Db 472 LLSGVLTIKLPETLGRIATWEAAKL-----ESENESSKILLT 513

Search completed: July 3, 2003, 12:42:37  
Job time : 53 secs

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|    |      |  |      |
|----|------|--|------|
| Db | 541  | TGCTCATGTCACCGAGTTTAACTGTAATGTGCCAACTCTCGATGTTGGACATTTC        | 600  |
| OY | 582  | ACCTCCCTTCTTCTGTAGCGGTCGCTCGGCTCTTGTCGCGGAGCGTGTAGAC           | 641  |
| Db | 601  | CAGTATCAGTAGTAATGTAGATTCCTTAATTTGGCTGTATAGTAATGGCTACATAGACAGC  | 660  |
| OY | 642  | AGGTTTGGAGGAAGAAGCTTCTCTTCGCAACCAATGGCTGTACAGACTGGCTTCAGCTTC   | 701  |
| Db | 661  | AGGTTTGGCGGTAAAGCTCTGCGCTCCCTCAACTAACAGTCCATTAAGCTCAGCTGAGATT  | 720  |
| OY | 702  | CTGCAGATTTTTCATCATCAGCTGGGAGATTCACGTGTATTTTGTACGCGGGCAGT       | 761  |
| Db | 721  | CTCATGGGCATTTTCCOCCACCTATTAAGTGTGATATTAATTTTTCGCTTAATCCAGACTG  | 780  |
| OY | 762  | GGCCAGATTCCTCAACTATGTGTAGCTTACGCTTCATCTAGACAGAAATTTCTGGCAATCA  | 821  |
| Db | 781  | GTACAGCAAAAGCGGCTGTAAATAGGCTCAATCCGATTCGATTAACGAATTTGTGGGGGAGA | 840  |
| OY | 822  | GTTCGTATATATTTCTCTCATTTAGGAAGTGCACATTTTTCGAGTGGCTATATGCTG      | 881  |
| Db | 841  | TATCGGAGAACAGTGGGGAATTTTATACCAAGTTGCTA---TACAGTGGGCTCTCGGTG    | 897  |
| OY | 882  | CTGCCACTGTGTGCTTACTTTCATCAGAGACTGGCGGATGCTGCTGCGCTGACGGTG      | 941  |
| Db | 898  | CTAGTGGGGTGGCTTACGCACTTCTCTCACTGAGGTGGTGTGCACTGCAATGTCTGTG     | 957  |
| OY | 942  | CGGGAGTGTGTGTGTCGCCGCTGTGGTGTTTCATTCCTGAAATCTCCCGATGGCTGATA    | 1007 |
| Db | 958  | CCCAACTTCTTCTTCTGTCTATTACTGTGTGCATATCGAATCTGCCAGGGTGGCTGATC    | 1017 |
| OY | 1002 | TCGCAGAGAAATTTAGAGAGGCTGAAATATCATCATCAAAAAGCTGCAAAAATGTACAAC   | 1061 |
| Db | 1018 | TCGCCGAATTAAGAAATGTGAAGCCATGAAATCATTAAGCAATCGCAAAAGAAATGGA     | 1077 |
| OY | 1062 | ACAGTGTACCAAGCAGTAGATATTTATTTCTGTGGAGAGCTAAATCCCTGAAGCAGAG     | 1122 |
| Db | 1078 | AAATTTCTTACCCGCTCCCTTCAGCGCTGAGACTTGAAGAGAAACGTGCCAAAGAAATTG   | 1137 |
| OY | 1122 | AAAGCTTTCATTTCTGACCTGTTTCAGACTGTGAATTTGCAATATACCTATTAATGTGCT   | 1187 |
| Db | 1138 | AAACCTTCATTTCTTGACTGTGGTGCAGAACTCCTCGAATTAAGAAACATATATGATTTG   | 1197 |
| OY | 1182 | TTGCGCTATAGATGCTACCTCAAGTGGGTTACTTGTCTGTCTGTGATGTCTCTAAT       | 1241 |
| Db | 1198 | ATGTACAACTGGTTCACAGCTCTGTGTCTTACCAAGGCGCTCATCATCAATGGGCGCTT    | 1257 |
| OY | 1242 | TTACATGAGATGCTTACCTCAACTGTTTCTCTCTGCTGCTGATTTGAATTCAGCTTAC     | 1301 |
| Db | 1258 | GCAGGTGACAAATATCTACCTGGATTTCTTCTACTCTGCTGTGTTGAATTCOCACGCTGC   | 1317 |
| OY | 1302 | ATTACAGCCTGTGCTATTTCGGAACGCTGCCAGGCGTTATATCATAGCTCAGATCTG      | 1361 |
| Db | 1318 | TTTCATGATCATCTCATATATGACCGCATCGCAGCGCTTACCTTGGGGCTGATCAATAT    | 1377 |
| OY | 1362 | TTTCGGGGAGAGGATGCTTCTCTGTCACTTAACTGATACCTGTGAGATTAATTACTTCTTA  | 1421 |
| Db | 1378 | ATGTTGTGAGGGGAGCGCTGTCTGCGCTCAAGTTTATTACTGTGATCTTAACAATGGCTTA  | 1437 |
| OY | 1422 | TCCAATGTGCTGTGATGCTGGGAAAAATTTGGGATCAACCTGTGCTTCTCCATGCTGAT    | 1481 |
| Db | 1438 | AAAATTTTATCTCATGCTGTGGAAGAAATGGGATACAAATGGCGCTATGAATATGTCTGC   | 1497 |
| OY | 1482 | GTCTTCACTGTGTAGCTCTTACCCCAACCTGTGTACAGAAATGCGCGTGGGGGTACATCC   | 1541 |
| Db | 1498 | CTGTCTCAATGTGTAGCTGTACCCCAATTCATTTAGGAATCTTTGGCGTCCACATCTGTTC  | 1557 |
| OY | 1542 | ACGGCTTCAGAGTAGGAGCAGCATTAATGGCCCCCTACTTGTATTAATCTCGGCTCAACAAC | 1601 |
| Db | 1558 | TCAATGTGTGCATTTGGGTGCATATCAAGCGCAATCTCTGTGTACCCGCTCATTAAATCTC  | 1617 |
| OY | 1602 | AGAAAT---GCTGCCCTTACATCGTCATGGGTATGTCTGACTGCTCGAATTTGAATCTTACC | 1658 |
| Db | 1618 | TGGCTTGAAGTCCCGCTGATGTGTCTTTCGGGGTACTTGGCTGTGGTGGAGGTCTGATG    | 1677 |

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Yy      1655 CTTTTHTTCCCGAAAAGTTGGGATGACTCTTCACAAAACCTTAGCGAGATGCGAGAA 1718
          || || || || || || || || || || || || || || || || || || || ||
Db      1678 CTGTGGCTTCACGAAAGAACTTAAGGGGAAAGCCTTGGCTTGAGACCATCGAGGAAGCGGAAAT 1737
          || || || || || || || || || || || || || || || || || || || ||

Yy      1719 GTGAATGTTTCAGATCTGGGAAAAAA 1746
          || || || || || || || || || || || || || || || || || || || ||
Db      1738 ATGCAGAAAGCAAGAAAAAATTAAGAAA 1765
          || || || || || || || || || || || || || || || || || || || ||

RESULT 2
US-09-040-444-6
: Sequence 6, Application US/09040444
: Patent No. 6063766
: GENERAL INFORMATION:
: APPLICANT: Koepsell, Hermann
: APPLICANT: Grundeman, Dirk
: TITLE OF INVENTION: Transport of protein which effects the
: TITLE OF INVENTION: Transport of cationic xenobiotics and/or pharmaceuticals
: TITLE OF INVENTION: DNA sequences encoding it and their use.
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner, L.L.P.
: STREET: 1300 I Street, N.W., Suite 700
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/040,444
: FILING DATE: March 18, 1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: O'Connor, Steven P
: REGISTRATION NUMBER: 41,225
: REFERENCE/DOCKET NUMBER: 2481.1453-01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)408-4000
: TELEFAX: (202)408-4400
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1896 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-09-040-444-6

Query Match      9.1%; Score 195.2; DB 3; Length 1896;
Best Local Similarity 48.5%; Pred. No. 3.6e-40;
Matches 596; Conservative 0; Mismatches 626; Indels 6; Gaps 2;

Yy      522 TCCACGCTGTGACCGAGTGAATCTGCTGTGAGAGACAACCTGGAAGTGCCTCAC 581
          || || || || || || || || || || || || || || || || || || || ||
Db      541 TCGTCACATGTCACCGAGGTAACTGATGTGCCAACCTCGATGTTGACCTATTC 600
          || || || || || || || || || || || || || || || || || || || ||

Yy      582 ACCTCCATGTTCTTCTGAGGCGTGCCTCGGCTCTTCTGCTCCGGGACGCTGCAGAC 641
          || || || || || || || || || || || || || || || || || || || ||
Db      601 CAGTCACATGATGATGAGAGATCTTATATGTGCTATGATAGATATGGCGTACATACAGAC 660
          || || || || || || || || || || || || || || || || || || || ||

Yy      642 AGGTTTGGCAGGAAGACGTTCTCTTCCGACACCAAGGCTGTACAGACTGCTTACGCTTC 701
          || || || || || || || || || || || || || || || || || || || ||
Db      661 AGGTTTGGCCGATGAGTCTGCGCTCCATACAGTCTTCATTAAGCTGACGCTGAGATT 720
          || || || || || || || || || || || || || || || || || || || ||

Yy      702 CTGCAGATTTTCTCCATGACGCTGGAGATGTTCACTGCTGATTTATGATGATGGGCAATG 761
          || || || || || || || || || || || || || || || || || || || ||
Db      721 CTATGAGCAATTTTCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
          || || || || || || || || || || || || || || || || || || || ||

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OY 762 GGCCAGATCTCCAACTATGATGCTTCACTAGAGAAATCTGGCAAGTCA 821
DB 781 GTGAGAAAGCAGGCTGTTAATAGCTACATCCGATTAACAGAAATTTGTTGGGGAGCA 840
OY 822 GTTCGATTATATTTCTCTACATTAGAGATGTCACATTTTTCAGTTGGCTATATGCTG 881
DB 841 TATCGGAGAAAGTGGGGATTTTTCACAAAGTTGCTA---TACAGTTGGGCTCCGGTG 897
OY 882 CTGCACTGTTGCTTACTTCACTACAGAGCTGGCGGATGCTGCTGGCGCTGACGGTG 941
DB 898 CTGAGTGGGGTGGCTTACCCACTCTCCACATGGAGGCTGCTTCACTGCTGCTG 957
OY 942 CCGGAGTGTGTGTGCTCCCGCTGATGCTGCTTCACTGAAATCCCGGATGCTGATA 1001
DB 958 CCCAATCTTCTTCTTCTGCTTATTAATCTGTGATACCTGAGTCTCCAGGCTGATNC 1017
OY 1002 TCCCAAGAGATTTAGAGAGGCTGAGATATCATCCAAAAGCTGCAAAAATGAAACAC 1061
DB 1018 TCCCAAGATTAAGATCTGAGGATGAGATCATTAAGACATCGCAAAAAGAAATGGA 1077
OY 1062 ACAGCTGTACCAAGCAATGATTTGATTTCTGTGAGAGACTAAATCCCTGAAAGCAG 1121
DB 1078 AATCTCTACCCGCTCCCTTACGCGCTGAGACTTGAAGAGGAACTGGCAAGAAATG 1137
OY 1122 AAGCTTTTCACTTCTGAGACCTGTTCAGAGACTCGGAATATGCGATATGACATTAATGCT 1181
DB 1138 AACCTTTCATTTTTCGATTTGCTGATGCTGATACCTCCATATAGGAAATATGATGATG 1197
OY 1182 TTGCTGTATGATGCTGATGACCTGAGGCTGATGCTGCTGCTGCTGATGCTGCTGAT 1241
DB 1198 ATGTACAACTGTTTACAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1257
OY 1242 TTACATGAGAGATGCTTACCTGAACTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 1301
DB 1258 GCAGGTGACAAATCTACCTGATTTCTTCTACTGCTGCTGCTGCTGCTGCTGCTGCT 1317
OY 1302 ATTACAGCTGCTGCTGATTTGCAAGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 1361
DB 1318 TTGATGATCATCTCTCATATACAGCCGATGAGAGCGGCTTACCTTGGGCTGATCAAT 1377
OY 1362 TTCTGGGAGAGGCTGCTGCTGCTTCTTCAATTCAGCTGATGCTGCTGCTGCTGCT 1421
DB 1378 ATGCTGACAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1437
OY 1422 TCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1481
DB 1438 AAAATTTATTTCTCATGCTTGGGAGAGATGCGGATGCAATGCTGCTGCTGCTGCT 1497
OY 1482 GTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1541
DB 1498 CTGCTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1557
OY 1542 ACGGCTTCAAGAGTGGGAGCATATTCGCCCTTACTTGTGCTGCTGCTGCTGCTGCT 1601
DB 1558 TCAATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
OY 1602 AGAAT---GCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1658
DB 1618 TGGCTGAGCTCCCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1677
OY 1659 CTTTTCCTTCCCTGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1718
DB 1678 CTGCTGCTTCCAGAAATTAAGGAAAGCTTTCGCTGAGACCATCGAGGAAAGCGGAAAT 1737
OY 1719 GTGAATGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1746
DB 1738 ATGCAAGACCAAGAAAAAATAAGAAA 1765

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RESULT 3  
 ; Sequence 4, Application US/08501572

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; Patent No. 6063623
; GENERAL INFORMATION:
; APPLICANT: Koepsell, Hermann
; APPLICANT: Grundeman, Dirk
; APPLICANT: Gorboulev, Valentin
; TITLE OF INVENTION: Transport of protein which effects the
; TITLE OF INVENTION: Transport of cationic xenobiotics and/or pharmaceuticals,
; TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Finegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,572
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Toohey, Kimberlin M
; REGISTRATION NUMBER: 35,391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)408-4000
; TELEFAX: (202)408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1882 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-501-572-4

Query Match 8.2%; Score 175; DB 3; Length 1882;
Best Local Similarity 47.5%; Pred. No. 5,1e-35;
Matches 585; Conservative 0; Mismatches 640; Indels 6; Gaps 2;

OY 522 TCCACCGTCTGATCCGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 581
DB 434 TCCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 493
OY 582 ACCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 641
DB 494 CAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
OY 642 AGGTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
DB 554 AGGTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 613
OY 702 CTGCAAGTTTCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
DB 614 CTACAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 673
OY 762 GGCCAGATTTCCAACTATGATGCTTCACTAGAGAAATCTGGCAAGTCA 821
DB 674 GTGAGAAAGCAGGCTGTTAATAGCTACATCCGATTAACAGAAATTTGTTGGGGAGCA 730
OY 822 GTTCGATTATATTTCTCTACATTAGAGATGTCACATTTTTCAGTTGGCTATATGCTG 881
DB 731 GGCTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
OY 882 CTGCACTGTTGCTTACTTCACTACAGAGCTGGCGGATGCTGCTGGCGCTGACGGTG 941
DB 791 CTGCGGGGCTGCTTACCCACTCTCCACATGGAGGCTGCTGCTGCTGCTGCTGCTGCT 850

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OY      942 CCGGAGAGCTGTGTGGCCCGCTGGTGGTGTAATTCCTGGAAATCTCCCGATTGGCTGATA 1001
|         |||||
Db      851 CCTACCTTCCTCTCCTCTGTAATTACTGGTTTTGGCCAGATATCCCCGGGTGCTGTGG 910
OY      1002 TCCGAGAGAAGATTTAGAGAGGCTGMAAGATATCATCCAAAAGCTGC AAAAATATACAAC 1061
|         |||||
Db      911 TCCCGAAGAGAACACCACCGAGCTGTGCAGATTAATGAGCAAAATTGGCACAGAAAGGGG 970
OY      1062 ACAGGTGTACCAAGACAGTATATTTGATTTCTGTGGAGAGCTAAATTCCTGTAAGCAGAG 1121
|         |||||
Db      971 AAGTGCCCTCCCTGGCTGACCTTAAGATGCTGTGCCCTTAGAGGAGATGGCTCGAAAAACGA 1030
OY      1122 AAAGCTTTCATTTCTGGAGACTGTTCAGACACTGGAAATATATGCCAATATGACCATATGCT 1181
|         |||||
Db      1031 AGTCCTTGCTGTGGCGAGACTGTGTCCGACACTCCCAACCTGAGAGAACACACCGTATCTGT 1090
OY      1182 TTGCTGCTATGGATGCTGACCTCAAGTGGGTACTTTGCTGTCTGTGTGGATGCTCTPAAT 1241
|         |||||
Db      1091 ATGATATCATGTTGTTCTTGTGGTGTGCTGACAGGCTGTCCATCATGACAGCTGGAGACC 1150
OY      1242 TTACATGAGATGGCTACCTACCTACATGTTTCTCTGCTGGCTGATTGAAATTCAGACTAC 1301
|         |||||
Db      1151 ACAGGGGCGCAACCTCTACCTGACTTCTTTATTTCTCTCTGGTGGAAATTCGCCGGGCC 1210
OY      1302 ATTACAGCTTGCTGCTATTGCGAAGCTGCGCCAGGCGTATATATCATAGCTGCAGTACTG 1361
|         |||||
Db      1211 TTCATCATCTCGTGACCATATGACCGGATTTGGCCGACATCTACCAATATGGCGCTCGAAT 1270
OY      1362 TTCGGGGAGAGGAGTGTGCTTCTCTTCATTAACATGGAGACTGTGATTAATTCCTCTTA 1421
|         |||||
Db      1271 CTGTGTAGAGGGGGGACGCTGCTCTCTCATGATCTTTATCCGCAATGACGTGCAGTGGTG 1330
OY      1422 TCCATTTGCTGTGATGCTGTGGAAAAATTTGGATCACTCTGTCTTCTCCATGCTGTAT 1481
|         |||||
Db      1331 AACCTTACCCCTGCGCTGTCTTGTGGCGGTATGGGGCCACATTTGHTGCTGAGATGGCTGC 1390
OY      1482 GTCTTCACCTGTGTAGCTCTTACCCCAACCTGTGTCAGAAACATGGCGGTGGGGTGCATCC 1541
|         |||||
Db      1391 CTGTGTAGACGTGTAGCTGTATCCCTACATTCATTCAGGAATCTTGGAGATGAGGATGTGCT 1450
OY      1542 ACGGCTCCAGAGTGGGAGCAGCATATGCCCCCTACACTTTGTTTAC--CTCGGTGCTTAC 1598
|         |||||
Db      1451 GCCCTGTGTGACTGTGGTGGGATGTTCAACCCCCTTATGATGTTCAAGCTGATGAGAAATT 1510
OY      1599 AACGAAATGCTGCCCCCTACATGCTGATGGGATGAGTGTACTGTCTCTGATTTGSAATCTTACC 1658
|         |||||
Db      1511 TGSCAAGCCCTGCCCCCTCATTTGTTTGGGATTTTGGGCGCTGACTGCTGGGGCCATGACT 1570
OY      1659 CTTTCTTTCCCTGAAATTTGGGAATGACTCTTCCAAACAACTTAGAGCAGATGACGAAA 1718
|         |||||
Db      1571 CTCCTTCTCCAGAGACCAAGGCTGTGGCTTTGCTGTAGACTATTTGAAGAAGACAGAGAAC 1630
OY      1719 GTGAATGCTTACAGATCTGGGAAAAAACAA 1749
|         |||||
Db      1631 CTGGGAGAGGAAGAAATCAAAGCCAAAGAAA 1661

RESULT 4
US-09-040-444-4
Sequence 4, Application US/09040444
Patent No. 6063766
GENERAL INFORMATION:
APPLICANT: Koepsell, Hermann
APPLICANT: Grundeman, Dirk
APPLICANT: Gorboulev, Valentin
TITLE OF INVENTION: Transport protein which effects the
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan,Henderson,Farabow,Garrett & Dunner, L.L.P.
STREET: 1300 I Street, N.W., Suite 700
City: Washington
```

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1 STATE: D. C.
2 COUNTRY: USA
3 ZIP: 20005-3315
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patentin Release #1.0, Version #1.30
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/09/040,444
11 FILING DATE: March 18, 1998
12 CLASSIFICATION:
13 ATTORNEY/AGENT INFORMATION:
14 NAME: O'Connor, Steven P
15 REGISTRATION NUMBER: 41,225
16 REFERENCE/DOCKET NUMBER: 2481.1453-01
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (202)408-4000
19 TELEFAX: (202)408-4400
20 INFORMATION FOR SEQ ID NO: 4:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 1882 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE: DNA (genomic)
27 US-09-040-444-4

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|             |       |            |       |              |
|-------------|-------|------------|-------|--------------|
| Query Match | 8.28; | Score 175; | DB 3; | Length 1882; |
|-------------|-------|------------|-------|--------------|

Matches 585; Conservative 0; Mismatches 640; Indels 6; Gaps 2;

522 TCCACCGTGTGACCGAGTGAATCTGGTGTGAGGACAACCTGGAAGTGCCCTCACC 581

Db 434 TCCTCCATCGTCACTGAGTTTAACTGGTGTGGAGACGCCCTGGAAAGTGGAACCTTTT 493

582 ACCTCCCTGTTCTTCGTAGGCGTGGCTCCTCGGCTCCTGTCGTCGGGCGAGCTGTCAGAC 641

Db 494 CAGTCTGTGTAAGTGGGCTTCTTCTGGGCTCCCTGGTTGTGGGTACATTGCAGAC 553

642 AGGTTGGCAGGAGACGTTCTCTTCGCAACCATGGCTGTACAGACTGGCTTCAGCTTC 701

Db 554 AGGTTGGCCGTAAGCTCTGTCTCTTGGTGACCAACGCTGGTCAATCTGTGTCCGGTGTG 613

702 CTGCAGATTTCTCCATCAGCTGGAGATGTTCACTGTATTGTGTCATCGTGGCATG 761

Db 614 CTACAGCGGTGGCCCGAGACTATACATCCATGTTGCTCTTTCGCTGCTGCAGGGCATG 673

762 GCCGATCTCCACTATGTGGTAGCCCTTCATACTAGGACAGAAATCTTGGCAAGTCA 821

Db 674 GTCAGCAAGGGCAGCTGGGTGTCGGCTATACCTTGATCAGAGAGTTGTCCGC---TCT 730

822 GTTCGATTATATCTCTACATTAGGAGTGTGCACATTTTTCGAGTTGGCTATATGCTG 881

Db 731 GGCTACAGGAGACGACGGCCATTTTGTACCAGATGGCCTTCACAGTGGGGCTAGTGGG 790

882 CTGCCACTGTTTGGCTTACTCATCAGAGACTGGCGGATGCTGCTGGCGCTGACGGTG 941

Db 791 CTGCGGGGTGGCCATTCAGACTGGCGCTGGCTCCAGCTAGCTGTGTCCCTG 850

942 CCGGAGTGTGTGTCCCGTGTGGTTCATTCCTGAATCTCCCGATGCTGATA 1001

Db 851 CCTACCTTCTCTTCTGCTGTAATTA CTGGTTTGTC CAGAAATCC CCGGTGGCTGTTG 910

QY 1002 TCCGAGAGAAGATTAGAGAGGCTGAAGATATCATCCAAAAAGCTGCAAAAAATGAACAAC 1061

Db 911 TCCAGAGAGAACCCACGCGAGCTGTCAGGATATGGAGCAATTGCCACAGAGAACGGG 970

1062 ACAGCTGTACCAGCAGTGATATTGATCTGTGGAGGAGCTAAATCCCTGAAGCAGCAG 1121

Db 971 AAGTGCCTCCTGCTGACCTGAAGATGCTCTGCCTTGAGGAGGATGCCCTCAGAAAAGCGA 1030

1122 AAAGCTTTCATCTGGACCTGTTGAGGACTCGGAATATTGCCAATATGACCATTAATGCT 1181

|  |      |   |      |
|--|------|---|------|
| Db   | 1031 | AGNCTTCGTTGGCCGACACTGTTCCGACATCCCAACCTGAGGAAACAAACCGCTATCTCGT | 1090 |
| QY   | 1182 | TTTGCTCTATGATGCTGACCTCAGTGGGTTACTTTGCTCTCTCTGATGCTCTTAT       | 1241 |
| Db   | 1091 | ATGATATCTATGTTGTTCTTGTGCTGTGCTACCAAGGGCTCATCATGACGACGTGGAGCC  | 1150 |
| QY   | 1242 | TTACATGAGGAGATCCATACCTGAAACGTTTCCCTGCTGATTTGAATTCACACTTAC     | 1301 |
| Db   | 1151 | ACAGGGGCCAACCTCTACCTGAGACTTCTTTATCTCTCTGTGTGAATTCGCCGGGCC     | 1210 |
| QY   | 1302 | ATTACAGCCTGAGCTGCTATTTGCGAACGCTGCCAGGCGTTATATCATAGCTGACGACTG  | 1361 |
| Db   | 1211 | TTTCATCATCTGTGTTACCATTTGACCGCATTTGGCCGCACTTACCAATACGCGCTCGAAT | 1270 |
| QY   | 1362 | TTGTTGGGAGGAGAGTGCTGCTCTCTCATTTCAACGTGCTACGCTGATATTAATCTTTA   | 1421 |
| Db   | 1271 | CTGTGTACGGGGACACCTGCTGCTCCATCATCTTATATCCGCAATGAGCTGCAGTGTG    | 1330 |
| QY   | 1422 | TTCAATGTTGTTGCTCATGCTGAGGAAATTTGGAGATACCTCTGCTTTCATGCTGTAT    | 1481 |
| Db   | 1331 | AAGCTTACCTCGCCGCTGTGTGGCCGTATGGGGGCCACCATGTTGCTGCAGATGGTCCG   | 1390 |
| QY   | 1482 | GTTCTTACTGTAGCTCTTACCAACCCGTGTACGAGAAATAGCGGTGGGGGTACATCC     | 1541 |
| Db   | 1391 | CTGTGTAAACCTCAGGTGTGATCACTTATCATAGGAAATCTTGGAGTATGATGTCTAT    | 1450 |
| QY   | 1542 | ACGAGCTCCAGATGGGAGACATCATTTGCCCTTACTTTGTTTAC---CTCGGTGCTTAC   | 1598 |
| Db   | 1451 | GCCTGTGTACCTGGGTGGGATCTTACACCCCTTATGTGTGTCAGGCTGATGGAAGTT     | 1510 |
| QY   | 1599 | AACAGAAATGCTGCCCTCATCTGCATGAGGTAGTGTGATGCTGATTTGAAATCTTACCC   | 1658 |
| Db   | 1511 | TGGCAAGCCCTGCCCTCATTTTGTGGGGTTTGGGCTGACTGCTGGGGCAGTACT        | 1570 |
| QY   | 1659 | CTTTTTTCCCTGAAAGTTTGGGAATGACCTTCCGAAACCTTAGAGAGATGCGAATA      | 1718 |
| Db   | 1571 | CTTCTTCTCCAGAGACCAAGGCTGTGGCTTTGCTCGAGACTTGAAGACGACGAGAAC     | 1630 |
| QY   | 1719 | GTAATATGTTTCAGATCTGGGAAAAAACA                                 | 1749 |
| Db   | 1631 | CTGGGAGAGAGAAATCAAGGCCAAGAAA                                  | 1661 |
| RESULT 5   |      |   |      |
| US-08-501-572-5  |      |   |      |
| Sequence 5, Application US/08501572  |      |   |      |
| Patent No. 6063623   |      |   |      |
| GENERAL INFORMATION:   |      |   |      |
| APPLICANT: Koepsell, Hermann   |      |   |      |
| APPLICANT: Grundeman, Dirk   |      |   |      |
| APPLICANT: Gorboulev, Valentin   |      |   |      |
| TITLE OF INVENTION: Transport Protein Which Effects The                      |      |   |      |
| TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals |      |   |      |
| NUMBER OF SEQUENCES: 6   |      |   |      |
| CORRESPONDENCE ADDRESS:  |      |   |      |
| ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner                    |      |   |      |
| STREET: 1300 I Street, N.W., Suite 700                                       |      |   |      |
| CITY: Washington   |      |   |      |
| STATE: D.C.  |      |   |      |
| COUNTRY: USA   |      |   |      |
| ZIP: 20005-3315  |      |   |      |
| COMPUTER READABLE FORM:  |      |   |      |
| MEDIUM TYPE: Floppy disk   |      |   |      |
| COMPUTER: IBM PC compatible  |      |   |      |
| OPERATING SYSTEM: PC-DOS/MS-DOS  |      |   |      |
| SOFTWARE: Patent Release #1.0, Version #1.30                                 |      |   |      |
| CURRENT APPLICATION DATA:  |      |   |      |
| APPLICATION NUMBER: US/08/501,572  |      |   |      |
| FILING DATE:   |      |   |      |
| CLASSIFICATION: 424  |      |   |      |
| ATTORNEY/AGENT INFORMATION:  |      |   |      |

[illegible]











QY 367 GCCGAGAGTGTCCACAGCTGACAGCCGCTACCGGCTGCGCCACCATCGCCAACTTTCGG 426  
DB 584 ACCACGAGGTGAAAGAGCCCTCTCCCGGCTCTGCGCCACATGAGAGCCACCGGGTAC 643  
QY 427 CGCTCGGCTGTGAGCCGGGGCGGACGCTGGGGGACGCTGGAGCAGAGAGCTGCC 486  
DB 644 GCGTGTGAGAGTGTCTTCCGCTTCCCTGTGAGAGCTGCGAGAGATCCGGCGCC 703  
QY 487 TGGATGCTGGAGTTCAGCCAGCCTACCTGCTCCACCTGCTGACGAGTGAATC 546  
DB 704 TCGAGAGAGAGTGTCTTCCGCTTCCGCGGCGCCACCTTCACTCACTCCCGGAGCAGC 763  
QY 547 TGGTGTGTGAGAGCACTGGAAGGTGCCCTCACCACCT 585  
DB 764 TGAAGAGGTGCTCTTGTGACGAGCTTAGGCTTCCGCGCT 802

RESULT 13  
PCT-US95-15327-3  
Sequence 3, Application PC/TUS9515327  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Biologically Active Fragments of  
TITLE OF INVENTION: Thermus Flavus DNA Polymerase  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15327  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28003/31716  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1794 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1794  
PCT-US95-15327-3

Query Match  
Best Local Similarity 2.6%; Score 55; DB 5; Length 1794;  
Matches 184; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 187 GGGGGCCCTTCAGCGCCTCATCTTCTCTGCTAGCGCCAGCATCCCAATGCT 246  
DB 404 GGGAGACCCCACTGCTCTGCTGCTAGAGCCCTTCAACACACACCCCGAGGGG 463  
QY 247 TCAATGTATGTACGTCTGCTTCTGCGGGGAGACCCGAGACCGCTGTGAGTGC 306  
DB 464 TGGCGGGGCTACGAGGGGGAGAGTACGAGAGACCGCCACACGCGGCGCTCTCTCG 523  
QY 307 ACGCCGGAACGTAGACGAGCGCTGCGGAGCAACAAGTGTCCGCTGCGGAGC 366

DB 524 AGAGCTCTCTGGAACCTCTTAACGCGCTCGAGGGGAGAGAAAGCTCTTGGCTCT 583  
QY 367 GCCGAGAGTGTCCACAGCTGACCGGCTACCGGCTGCGCCACATCGCCAACTTTCGG 426  
DB 584 ACCACGAGGTGAAAGAGCCCTCTCCCGGCTCTGCGCCACATGAGAGCCACCGGGTAC 643  
QY 427 CGCTCGGCTGTGAGCCGGGGCGGAGCGTGGAGCTGGGGGACGCTGAGCAGAGAGCTGCC 486  
DB 644 GCGTGTGAGAGTGTCTTCCGCTTCCCTGTGAGAGCTGCGAGAGATCCGGCGCC 703  
QY 487 TGGATGCTGGAGTTCAGCCAGCCTACCTGCTCCACCTGCTGACGAGTGAATC 546  
DB 704 TCGAGAGAGAGTGTCTTCCGCTTCCGCGGCGCCACCTTCACTCACTCCCGGAGCAGC 763  
QY 547 TGGTGTGTGAGAGCACTGGAAGGTGCCCTCACCACCT 585  
DB 764 TGAAGAGGTGCTCTTGTGACGAGCTTAGGCTTCCGCGCT 802

RESULT 14  
PCT-US95-14418-1  
Sequence 1, Application PC/TUS9514418  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: DNA Encoding a Thermostable DNA Polymerase Enzyme  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14418  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28003/32330  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3048 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 301..2805  
PCT-US95-14418-1

Query Match  
Best Local Similarity 2.6%; Score 55; DB 5; Length 3048;  
Matches 184; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 187 GGGGGCCCTTCAGCGCCTCATCTTCTCTGCTAGCGCCAGCATCCCAATGCT 246  
DB 1415 GGGAGACCCCACTGCTCTGCTGCTAGAGCCCTTCAACACACACCCCGAGGGG 1474  
QY 247 TCAATGTATGTACGTCTGCTTCTGCGGGGAGACCCGAGACCGCTGTGAGTGC 306

Db 1475 TGGCGGGGCTACGAGGGGGAGTGGAGGAGGAGCGCCGCCCGGCGGCTCTCTCGG 1534  
QY 307 AGCGCGGCAACCTGAGCAGCGCGCTGGCGCAACAGTGTCCCGCTGGCGGCTGCGGAGC 366  
Db 1535 AGAGGCTCCTATGGAACTCTTAAGCGCTCTGAGGGGAGAGAGAGCTCTTTGGCTCT 1594  
QY 367 GCCGCGAGTGGCCCAACAGCTGAGCGCTACCGGCTCGCCACCACTGCCAACTTCTCGG 426  
Db 1595 ACCACGAGGTGAAAAAGCCCTCTCCCGGCTCTGGCCCACTGGAGGCCACCGGGGTAC 1654  
QY 427 CCTCGGCTGAGAGCGGGGGCGGAGCTGAGCTGGGGAGAGTGGAGAGAGAGAGCTGCC 486  
Db 1655 GCGTGGAGCTGGCTTACCTGAGCGCTTCTCCCTGAGCTTGGAGGAGATCCGCGCC 1714  
QY 487 TGGATGCTGGAGTTCAGCCAGAGCTTACCTGCTCCACCGCTCGTAGCCGAGTGAATC 546  
Db 1715 TCGAGAGAGAGGTCTTCGCTTGGCGGGGCGACCCCTCAACTCAACTCCGGGACAGC 1774  
QY 547 TGGTGTGAGGACAACTGGAAGGTGCCCTCACCACCT 585  
Db 1775 TGGAAAGGGTGTCTTTGACGAGCTTAGGCTTCCGCT 1813

RESULT 15  
PCT-US95-15327-1

Sequence 1, Application PC/TUS9515327  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Biologically Active Fragments of  
TITLE OF INVENTION: Thermus Flavus DNA Polymerase  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15327  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gaas, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28003/31716  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3048 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 301..2805  
PCT-US95-15327-1

Query Match 2.68; Score 55; DB 5; Length 3048;  
Best Local Similarity 46.1%; Pred. No. 0.00025;  
Matches 184; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 187 GGGGGCCCTCCAGCGGCTATCTCTCTGCTCAGCGGAGATCAATCCCAATGGCT 246  
Db 1415 GGGACGACCCATGCTCTCTGCTTACCTCTGAGACCCCTCAACACACCCCGAGGGG 1474

QY 247 TCAATGATATGTAGTGTCTCTCTGCGGGGAGACCCCGAGCAACCCGCTGTGAGTGC 306  
Db 1475 TGGCGGGGCTTACGGGGGGAGTGGACGAGAGACGCGCCGCAACCGGCGCTCTCTCGG 1534  
QY 307 AGCGCGGCAACCTGAGCAGGGGCTGGCGCAACAGTGTCCCGCTGGCGGCTGCGGAGC 366  
Db 1535 AGAGGCTCCTATGGAACTCTTAAGCGCTCTGAGGGGAGAGAGAGCTCTTTGGCTCT 1594  
QY 367 GCCGCGAGTGGCCCAACAGCTGAGCGCTACCGGCTCGCCACCACTGCCAACTTCTCGG 426  
Db 1595 ACCACGAGGTGAAAAAGCCCTCTCCCGGCTCTGGCCCACTGGAGGCCACCGGGGTAC 1654  
QY 427 CCTCGGCTGAGAGCGGGGGCGGAGCTGAGCTGGGGAGAGTGGAGAGAGAGAGCTGCC 486  
Db 1655 GCGTGGAGCTGGCTTACCTGAGCGCTTCTCCCTGAGCTTGGAGGAGATCCGCGCC 1714  
QY 487 TGGATGCTGGAGTTCAGCCAGAGCTTACCTGCTCCACCGCTGAGCCGAGTGAATC 546  
Db 1715 TCGAGAGAGAGGTCTTCGCTTGGCGGGGCGACCCCTCAACTCAACTCCGGGACAGC 1774  
QY 547 TGGTGTGAGGACAACTGGAAGGTGCCCTCACCACCT 585  
Db 1775 TGGAAAGGGTGTCTTTGACGAGCTTAGGCTTCCGCT 1813

Search completed: July 5, 2003, 07:07:36  
Job Time : 99 secs



|    |      |  |      |
|----|------|--|------|
| QY | 305  | GGACGCGCGGAACCTTAGAGAGCGCCGCGGCAACAACATGTCGCCGCTCGCGTGGGGGA      | 364  |
| Db | 282  | GGACCGCGGAACCTTAGAGAGCGCCGCGGCAACAACATGTCGCCGCTCGCGTGGGGGA       | 341  |
| QY | 365  | CGGCGCGGAGGTGCCACAGCTGCAGCGCTACCGCGCTCGCCACCATGCGCCAACTCTTC      | 424  |
| Db | 342  | CGGCGCGGAGGTGCCACAGCTGCAGCGCTACCGCGCTCGCCACCATGCGCCAACTCTTC      | 401  |
| QY | 425  | GGCGGCTCGGGGCTGGANACCCGGGGCGGACGTGGAACTGGGGCAGCTGGAGCAGAGCTTG    | 484  |
| Db | 402  | GGCGGCTCGGGGCTGGANACCCGGGGCGGACGTGGAACTGGGGCAGCTGGAGCAGAGCTTG    | 461  |
| QY | 485  | CCGTGATGTGCTGAGGATTCAGCCAGAGACCTTCACGTGTACACGCTGTGACCGAGAGGAA    | 544  |
| Db | 462  | CCGTGATGTGCTGAGGATTCAGCCAGAGACCTTCACGTGTACACGCTGTGACCGAGAGGAA    | 521  |
| QY | 545  | TCGTGATGTGAGAGACATGTGAAGGTGCCCTCACACCTCCCTGTTCTCTGTGAAGCGT       | 604  |
| Db | 522  | CTGTGGTGTGAGAGACATGTGAAGGTGCCCTCACACCTCCCTGTTCTCTGTGAAGCGT       | 581  |
| QY | 605  | GCTCTCTCGGCTCTTCTGTCGTGCGGGAGCTGTACAGACAGTGTGGAGAGAAAGCTTCT      | 664  |
| Db | 582  | GCTGTGGGCTCTTCTTCAATTTACAGGGCAGCTGTACAGAGTGTGGCCGGAAGAAATGTCT    | 641  |
| QY | 665  | CTTCCGACCATGCGCTGTACAGACTGTGCTTCAAGCTTCTCGAGATTTTCTCCATCAGCTG    | 724  |
| Db | 642  | GTTCGTGACCAATGGGCATGTCAACAGAGCTTCCAGCTTCCGAGATTTCTCCAGAAATTT     | 701  |
| QY | 725  | GGAGATGTTCACATGTGTATTTGTCATGCTGGGCAATGGGCCAGATCTCCACATATGTGCT    | 784  |
| Db | 702  | TGAGATGTGTGTGTCGTCTTGTCTGTCTGTGTAGCATGTGGCCAGATCTCCACATATGTGCT   | 761  |
| QY | 785  | AGCCTTCACTAGGAACAAGAAATCTGTGGCAAGTCACTGTATTAATATCTCTACAT         | 844  |
| Db | 762  | AGCAATTTGTCTGGGGACAGAAATTTCTGGCAAGTCACTGTATTAATATCTCTACAT        | 821  |
| QY | 845  | AGGAGTGTGACATTTTGGAGTGGGATATGCTGTGGCCAGCTGTGTCTTACTATCAT         | 904  |
| Db | 822  | AGGATGTGTACATTTTATTTATGTACTTGTGTACTATGTGTGTGCGCACGTGTGTCTTACTCAT | 881  |
| QY | 905  | CAGAGACTGGCGGATGCTGTGCTGTGCGCTGTGACGCTGGCGGAGTGTGTGTCCCGCT       | 964  |
| Db | 882  | CCGAGACTGGCGGATGCTGTGCTGTGCGCGGTGACGATGGCGGGGTGTGTGTGGACT        | 941  |
| QY | 965  | GTGGTGTGTCAATTCCTGATCTCCCCGATGGCTGTATTCACAGAGATTTAGAGAGCC        | 1022 |
| Db | 942  | CTGGTGTGTCAATTCCTGATCTCCCCGATGGCTGTATTCCTGAGGACATTTGAAGAGCC      | 1001 |
| QY | 1025 | TGAAGATATCAATCCAAAAAGCTGCAAAAATGAACAACAGCTGTACAGAGCTGAAT         | 1084 |
| Db | 1002 | AGAGTGTATCAATCCGCAAGAGCTGCCAAGGCCAATGGGATGTGTGTGCTTCCATCATCTT    | 1061 |
| QY | 1085 | TGATTTCTGTGAG-----GAGCTAAATCCCTGTAGAGCAGCAAGAAAGCTTTCATTCTGA     | 1138 |
| Db | 1062 | TGACCCGAGTAGTTTCAAGACCTTAAGTTTCCAAAGAAAGCAGAGTCCCAACATCTCTGA     | 1121 |
| QY | 1139 | CCGTGTTCAGAGCTGCGATATTTGGCATTAATAGCAATATGTCTTGTGCTGTATGAGATGCT   | 1199 |
| Db | 1122 | TCTGTTCGAAACCTGTGAATATTCGGATGTGTACCATCTATGTCCATTAATATGTGTGATAC   | 1181 |
| QY | 1199 | GACCTCAGTGGGTTACTTGTCTGTCTCTGATGTGCTGATGCTTCAATTTACATGAGATGCTTA  | 1258 |
| Db | 1182 | CATATCAATGTGGGCTATTTTGGGCTTGTGCTTGTATCTCTTAATTCATTTGGAGCATCTT    | 1244 |
| QY | 1259 | CCGTGAACGTTCCTCTCTGCTGCTGTGATTTGAATTCAGCTTACATTTACAGCTGGCTCT     | 1318 |
| Db | 1242 | TGTGAACGTCTCTCTTCAAGGAGGTGAAGTCCACATATGTGTGTGCTGCTGCTCT          | 1301 |
| QY | 1319 | ATTTCGGAACGCTGCCACGCTTAATATAGCTGCAGATGCTTGTGTGGGAGGAGGCT         | 1378 |
| Db | 1302 | GCTGCATATTTTGGCCCGGCGCTATTCATGTGACCTGCTTCTTCCGTGGGTGGCAGTGT      | 1361 |
| QY | 1379 | GCTTCTCTTCACTCACTGTACCTGTGGATTAATTAATCTTTATTCATTTGGTCTGTGAT      | 1438 |

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|----|------|--|------|
| Db | 1362 | CGTTCCTCTTCACGAGCTGTGACCCCCACAGACTTGATATATTTGGCTACAGCTCTGGTAT    | 1421 |
| QY | 1439 | GCTGGGAAATTTGGGATCACCTCTGCTTTCTCCATGCTGATATGCTTCACTGCTGAGCT      | 1498 |
| Db | 1422 | GGTGGGGCAAGTTTGGAGTCAAGGGTGCCCTTTTCATGGCTACGTTACAGTACACAGCCGACCT | 1481 |
| QY | 1449 | CTACCCAAACCTGGCAGAGAACATGGGGGGTGCATCCACAGGCTCCAGAGTGGG           | 1558 |
| Db | 1482 | GTAATCCACAGCTGGTGAAACATGGGGTGTGGAGTCACTCCACAGATCCCCGCTGGG        | 1541 |
| QY | 1559 | CAGCATCATTTGCCCTACTTGTTTTAACTGGGTGCTTACAACAGAAATGCTGCCCTACAT     | 1618 |
| Db | 1542 | CAGATATCTGTCTCCACTCTGTTACTCGTTTACTTGGTGCTCAGACCGGCTTCCGCTCTACAT  | 1601 |
| QY | 1619 | CGTCATGGGATGTGTGACTGTCTCGATTGGAATCTCACCCCTTTTTCCTGGAAGTTT        | 1678 |
| Db | 1602 | TCTCATGGGAAGTGTGACACATCTGACAGCCATCCTCACTTGTTTCTCCAGAGAGCTT       | 1661 |
| QY | 1679 | GGGATATGATCTTTCAGAAACCTTAGACAGATCAGAAAGTGAATGGTTACATCTGG         | 1738 |
| Db | 1662 | CGGTACCCCACTCCAGACACCATTTGACAGACATCTAAAGTCAAGAGATGAACAACAG       | 1721 |
| QY | 1739 | GAAAAAACAAGAGACTCAATGAGACAGAGAAAAATC                             | 1776 |
| Db | 1722 | AAAAATCTCCAGTCAACAGAGATTTAAAAAGATGGTC                            | 1759 |

## RESULT 2

US-09-798-743A-4

; Sequence 4, Application US/09798743A

Patent No. US20020099093A1

; GENERAL INFORMATION:

APPLICANT: NEZU, JUN-ICHI

APPLICANT: Use, Asuka

1. TITLE OF INVENTION: SYSTEMIC CARNITINE DEF  
2. REFERENCE: 06501-073001

FILE REFERENCE: 00501-0/3001  
CURRENT APPLICATION NUMBER: HS/09/7898 7432A

CURRENT AFFILIATION NUMBER: 05/0  
CURRENT FILING DATE: 2007-03-02

PRIOR APPLICATION NUMBER: PCT/JP99/048

PRIOR FILING DATE: 1999-09-07

PRIOR APPLICATION NUMBER: JP 10-252683

PRIOR FILING DATE: 1998-09-07

NUMBER OF SEQ ID NOS: 31

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; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 4

; LENGTH: 1888

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; TYPE: DNA

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; ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

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; LOCATION: (60)..(1730)
ms 00 700 743

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US-09-798-743A-4

Answer: Match

|                      |        |         |
|----------------------|--------|---------|
| Query Match          | 46.6%; | Score 9 |
| Post Local Citations | 75.78  | Score 3 |

Best Local Similarity 15.7%; Pred. N Matched 1247; Computation 0; Miss

mal'icines 1241; conservative 0; Mississ

130 GAGCGGCACTGGCGAAGCATGGCGGCACT

[illegible]

43 GGGAGCTGAGGACGGCATGGGGACTT

**T**

190 GGGCCCTTCACGGCCCTCATCTTCTTCC

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Db 103 GGGCCCTTCCAGCGCCCTCATCTTCTTCC

[illegible]

250 ATGGTATGTCAGTCGTGTTCCCTGGCGG

1. The first group of students (Group A) was assigned to read the text and identify the main idea of the passage. They were then asked to write a short paragraph summarizing the main idea in their own words.

Db 163 ATGGTATGTCATCGTGTTCCTGCGG

310 CCGCGAAGCTGAGCAGCGCCTGGCGCA

D<sub>b</sub> 223 CCGTGAACCTGAGCAGCGGTGGCGCA

Db 223 CCGTGAACCTGAGCAGCGCGTGGCGCAACCAAGTATCCCGTTGGAGACGAAGGACGAC 282



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QY 1589 CGGTGC-TTACAACAGATGCT-GCCCTACATGTCATGGTAGTCTGATGTCGATG 1646
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Db 520 GGATCTTCACCCCTTTTTCCTGAAAGTTTGGGAATGACTCTTCAGAAACCTTAGA 461
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QY 1706 GCAGATGCAGAAAGTGAATGGTTGATCTGGGAAAAAACAAGAGACTCAATGAGAC 1765
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Db 460 GCAGATGCAGAAAGTGAATGGTTGATCTGGGAAAAAACAAGAGACTCAATGAGAC 401
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Db 340 AAGTGAATAACAAAAATGAACCCCTGGGAGAAATTTGTTGCCCTGAAATGAGC 281
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Db 280 TGACTGTAAAGATTGACACCAAAATGAACTGTATCAAGAAATGCTGTATGAGTA 221
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QY 1946 AACTCTGATGATTTCTCCAGATGATGCTGCTTTTACAAACCAACATTTCTAGAG 2005
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QY 2006 TCTCTTACTCATTTAATGAATGAATGATGTAAGTGTCTTGAACCAACATGTTAGT 2065
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QY 2066 AAGAGCTGTAAATATCATATTAAGATTAACTACTATTTCCAATCATCAATATCTATCC 2125
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Db 40 AATATAAAT 31
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## RESULT 4

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US-09-798-743A-5
; Sequence 5, Application US/09798743A
; Patent No. US2002009903A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; APPLICANT: Ose, Asuka
; TITLE OF INVENTION: SYSTEMIC CARNITINE DEFICIENCY GENE AND USES THEREOF
; FILE REFERENCE: 06501-073001
; CURRENT APPLICATION NUMBER: US/09/798,743A
; PRIOR APPLICATION NUMBER: PCT/JP99/04853
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: JP 10-252683
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 25871
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (24071)..(24443)
; NAME/KEY: exon
; LOCATION: (24444)..(25871)
; US-09-798-743A-5

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Query Match 17.0%; Score 363.8; DB 10; Length 25871;
Best Local Similarity 92.3%; Pred. No. 4.7e-100;
Matches 383; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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QY 125 TTTCGAGCGGCACTGGGAAGCATGCGGACTACAGACGAGTATGCTCTCTGGGCGA 184
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Db 200 TCTGTGGGCTCTGTAGGGCGCATGCGGACTACAGACGAGTATGCTCTCTGGGCGA 259
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QY 185 GTGGGGGCGCTTCCAGGCGCTCATCTTCTTCTGCTCAGGCGACGATCATCCCAATGG 244
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Db 260 GTGGGGGCGCTTCCAGGCGCTCATCTTCTTCTGCTCAGGCGACGATCATCCCAATGG 319
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QY 245 CTTCAATGATATGATCTGCTGTTCTGCGGCGGACCCGAGACACCGCTGTGAGTGGC 304
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Db 320 CTTCAACGGGCTGTGCTGCTGTTCTGATAGGAGACCCGAGACACCGCTGTGAGTGGC 379
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QY 305 GAGCGCGGCAACCTGAGCAGCGGCTGCGGCAACAAAGTGTCCGCTGGGCTGGGGA 364
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Db 500 GCGGCTCGGCTGAGCGCGGCGGCGAGCTGAGCTGTGGGCACTGAGCAGAGAGAGCTG 559
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 485 CTTGATGGCTGGGAGTTCAGCCAGGAGGCTTACCTGTCCACCTGTGTAACGAG 539
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 TCTGATGGCTGGGAGTTCAGTCAAGGAGCTTACCTGTCCACCTGTGTAACGAG 614
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## RESULT 5

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US-09-284-320-30
; Sequence 30, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705C9US
; CURRENT APPLICATION NUMBER: US/09/284,320

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|----|------|---|------|
| Db | 867  | ATCTGTTTAAATCGTAGAGCATTTACGAAAGACACTTACCGTTTGGCTATATCGGTTCA       | 926  |
| OY | 1198 | TGACCTTCAGTGGGTTACTTTGCTGTGCTCTGTGATGCTCCTAAATTTACATGAGAGTCCCT    | 1257 |
| Db | 927  | CTGGAAGTTTGGGATCTTACTCGTTTTCCTTGAATCTGTAACTGTAGAGGCAATGAT         | 986  |
| OY | 1258 | ACCTGAACCTGTTTCCTCTCTGCTTGTGATTTGAATTTCAAGCTTACATTTACAGCTGCTGC    | 1317 |
| Db | 987  | ACTTAAACCTCTTCCTCTCTGCTGATGTGAAAAATCCCGGCTTACACCTTGTGTCATCG       | 1046 |
| OY | 1318 | TATTGCAAGCGTCCCGGAGCGGTTATATCATAGCTGTGAGTACCTGCTCTGGGAGAGAGGTG    | 1377 |
| Db | 1047 | CCATGACAAAGTGTGGGAGGAGAACAGTCCCTGGCTTACTCTCTTTCTGCACTGCACTGG      | 1106 |
| OY | 1378 | TGCTTCTCTTCAATCAACTGTATCTGTGATTTATTTACTTTTATCCATTGCTGTGCTCA       | 1437 |
| Db | 1107 | CTGTGTGTGTCGTTATGTGTATGTCATCCCGAAGAACTTATATTTTGGTGTGTGACACTGA     | 1186 |
| OY | 1438 | TGCTGGGAAAAATTTGGGATCACCTCTGCTTTCTTCATGCTGTATGTCTTCACTGCTAGAC     | 1487 |
| Db | 1167 | TGTTTGGAAAAATTTGGCATCGGGGACACATTTTGGCCCTCATATTTATCTTTATACACACTAGC | 1226 |
| OY | 1498 | TCTACCCACACCTGTGTGAGAACATGCGGGGTGAGGAGTCCACATCCAGGCGCTCCAGAGTG    | 1557 |
| Db | 1227 | TGTTTCCAAACATTTGTATAGATCGCTGCTGTGGGAAACGCGACAGATGTGTGCTGCTGG      | 1286 |
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| Db | 1287 | CCACATCATCGGGCGCGCTTCTGTGTGACCTCACACACATTTGATCTCTCATACACAGCT      | 1346 |
| OY | 1618 | TCTGTCATGGGTAGTCTGACTGTCTGATTTGGAACTTTCACCCCTTTTTTCCCTGAAGTT      | 1677 |
| Db | 1347 | TGTTTGTGGAGACTATGTGCCCTCCTGTAGTGTGAGTGTAACTTAAAGCTTCCAGAAACCC     | 1406 |
| OY | 1678 | TGGGAATGACCTTCCAGAAACCTTAGACGAGATGCAAGATGAAT                      | 1725 |
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|    | Only Match            | 6.5%  | Score 138         | DB 9      | Length 1431 |
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|    | Best Local Similarity | 47.3%   | Pred. No. 2,5e-31 |           |             |
|    | Matches 608           | Conservative 0  | Mismatches 645    | Indels 33 | Gaps 5      |
| QY | 454                   | TGACCTGGGGCAGCTGCAGCAGAGAGACTCCCTGATGCGCTGGAGATTGACCCAGCAGC     |                   |           | 513         |
| Db | 2                     | TGGAGGTGGAGGAGGCGCTTCACGGGCGTGGGGGAGAAAGTCATCTCCAGATGATTAATGTGT |                   |           | 61          |
| QY | 514                   | TCTACCTGTCACCGCTCGTGCAGCAGTGGATTCGTGTGTGAGGACAACTGGAAAGTGC      |                   |           | 573         |

|   |   |      |   |       |
|---|---|------|---|-------|
| D | b | 62   | GCCTTCGCTGGCCGCTCTGCTGCAGAGCGTTTAACTTGGCCAAAGATCTCATCAAGTCA     | 121   |
| Q | y | 574  | CCCTCACCACCTCCCTCTGTTCTGCTAGACCGCTGCTCCTCCGCTCTGCTGCGGACG       | 633   |
| D | b | 122  | GTGAGCAACGCTCTTTTCTCTCAGTGGTGTATTTGTTGGAGTATCTCTTTGGTCAGC       | 181   |
| Q | y | 634  | TGTCAGACAGGTTTGGCAGGAAAGAGCTTCTCTTCCACCAATGCGTGTACAGACTGGCT     | 693   |
| D | b | 182  | TTTCAGATGCCCTTCGAAAGGAAAAAAAGTCTATCTCACAGGTTTGGCTCTGACATCTTAT   | 241   |
| Q | y | 694  | TCAGCTTCGCGCAATTTTCTCATCAGCTGGGAGATGTCACGTGTATTTGTCTATCG        | 753   |
| D | b | 242  | TTGCAATTCGCAATGAGATTTTCCCTCCATATAGTGTCTTTGACGTAACTGCTCTCGG      | 301   |
| Q | y | 754  | TGGCATGGGCGAGATCTCCAACTATGTGGTAGCTTCATACTAGAAACAGAAATTCCTG      | 813   |
| D | b | 302  | TGGGCATGATGAATGAGAGGATGTGCGTGGGCGCTTGTCTCTCTTAAGAAATGTGG        | 361   |
| Q | y | 814  | GCAAGTCAGTTCGTATTATTAATCTCTACATTTAGAGTGTGCACATTTTGTGCACTGGCT    | 873   |
| D | b | 362  | GCA---CCGCGTACTGGGCACTTGCAAGATCGATTTGGCGGCGCTCTCTTGAGTTGGCA     | 418   |
| Q | y | 874  | ATATGCTGCGGCACTTTTGCTTACTTCACTCAAGACACTGGCGGATGCTGCTGTGGCGC     | 933   |
| D | b | 419  | TTGCCCCAATATGCCCTGTAGAGTACTTCATCCGCTCTTGAGGACCTTACCATTTCTGG     | 478   |
| Q | y | 934  | TGACGCTGCCGCGAGTCTGTGTGTGCCGCTGTGGTGGTTCATCTCGAAATCTCCCAT       | 993   |
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| Q | y | 1114 | AGCAGCAAAAGCTTTCAATCTGGACCTGTACAGACTCGGAATATTCATTAATGACCA       | 1173  |
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| Q | y | 1174 | TTATGCTTTTGTCTGCTATGATGCTGACCTCAGTGGGTTACTTGTCTGTCTCTGGATG      | 1233  |
| D | b | 713  | TGATCGATGATGTTATCTGTTTGTGTGGACGCTTGGTGATTAATGAGGCTAACTGTAGTG    | 772   |
| Q | y | 1234 | CTCTAAATTTACATGAGATGCTTACTGAACTGTTCCTCTCTGCTTGATTTGAAATTC       | 1293  |
| D | b | 773  | CGGCTGATCTAGGTGGAAGTATTTATGCAACTGGCCCTGTGCGCTCATAGAGATTC        | 832   |
| Q | y | 1294 | CAGGTTAC---ATTACAGCGCTGGGTATTTGCGAAGCGTCCGACGGGATTAATTCATAG     | 1350  |
| D | b | 833  | CATTTTACCCTCTCTGTATCTACTTGATTAACCAAAAATGGTTTGTGGGAAGCGAATAT     | 892   |
| Q | y | 1351 | CTGCAATGCTGTTCTGGGAGAGAGTGTGCTCTCTTCAATCAACTGTAACCTGTGATTT      | 1410  |
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| Q | y | 1450 | TTGGGATACACTGCTGCTTCTTCCATGCTGTAATGCTATCTACAGTGCAGACTCTAACCAACC | 1509  |
| D | b | 1013 | TGACCATCATGCTGCTTTAACATTTTATTTATTTTCTTACCTCTTGACCTTTTACCTCTACG  | 10722 |
| Q | y | 1510 | TGCTCAGGAACATGCGGTGGGGGTTCATATCCAGGCGCTCCAGAGTGGGCGAGCATATYG    | 1569  |
| D | b | 1073 | TCATCAGGAATGTTGGGCTTGGAACTGTTCATGTTCTCCGAGTTGGTGGGATTAATTTG     | 11322 |
| Q | y | 1570 | CCCCCTACTTGTGTTTACCTGGTGTTCACAAAGAAATGTGCCCTCATGTCATGAGGTA      | 1629  |





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Db      624  CCACCCGTCGCGGGGCTGAACCACTGCGTCTCTTGCATGTATGAGTGAGGCGGCGACG 683
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Db      684  GGGCGGACCTTGGTGATGACCTTAACCTCTCTGGGCTTCAAGCTTGGCCATGGGCTTAC 743
Oy      877  TCCCTGCTGCACACTGTTTCTTACTTCAACAGAGACAGTGGCGGATGCTGCTGCGCTGA 936
Db      744  AACTGCAG-----TGGCTACGGGTGCGGAGTGGACACTGCTGCAGCTGGTGGTCT 796
Oy      937  CGGTGCGGAGAGTGTGTGTCTCCGCGTGGTGTATCTCCGAATCTCCCGAGTGGC 996
Db      797  CGGTGCGGAGAGTGTGTGTCTCCGCGTGGTGTATCTCCGAATCTCCCGAGTGGC 856
Oy      997  TGTATATCCAGAGAGATTATAGAGG-----CTGAAGATATATATCC 1038
Db      857  TCTTCACACAGAGGCGTGGATTTGGGCGCTGCAGAGAGCTGTGAGGGTGGCTCCATCA 916
Oy      1039  AAAAACTGCATAAATGAACAACACAGCTGTACAGCAGTGTATTTGATTTCTGTGAGG 1098
Db      917  ACGGAAGGGGGAGTGCAGAGACACCTGACCCCTGAGGTCTTGTCTTCAAGCATGCGGG 976
Oy      1099  AGCTAATCCCTGGAAGCAGACAGAAAGCTTTCAATCTGACCTGTTCAGAGTCCGAAATA 1158
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Db      1037  TGGGCTTCCGAGCATGTATCTCCAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
Oy      1219  CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1278
Db      1097  GCTTGGGCTGAGCTGAGCTGAGGCGCTTGGGAGAGAACTCTCTGCTCCAAATGTTTATG 1156
Oy      1279  CCTTGAATTAATTCAGCTTACATTAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1338
Db      1157  GTGTGCTGAGCATCCAGCAGCAAGATGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1216
Oy      1339  GTTATATCAATGAGTGTAGTACTGTGTGAGGAGAGTGTGCTGCTGCTGCTGCTGCTGCTG 1398
Db      1217  GCGCCGAGCTGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1276
Oy      1399  TACCTGTGATTTATTAATCTTATTCATTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1458
Db      1277  TGGCCCAAGAAATGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1336
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Db      1337  GGGCTGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1396
Oy      1519  ACATGGGAGTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1578
Db      1397  TGAAGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1456
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Db      1457  TCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1516
Oy      1639  TCTGATTTGGAATCTTACCTTTTTCCTGGAAGTTTGGGAATGAGCTTCCGAGAA 1698
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RESULT 12  
 US-10-095-139-4  
 : sequence 4, Application US/10095139  
 : Patent No. US20020165357A1  
 : GENERAL INFORMATION:

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: APPLICANT: Curtis, Rory A.J.
: APPLICANT: Silos-Santiago, Immaculada
: TITLE OF INVENTION: Millennium Pharmaceuticals, Inc.
: TITLE OF INVENTION: Ion Transporters and Uses Therefor
: FILE REFERENCE: MP101-0171P1RM
: CURRENT APPLICATION NUMBER: US/10/095,139
: PRIOR FILING DATE: 2001-03-12
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 2866
: TYPE: DNA
: ORGANISM: homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (365)...(2026)
: OTHER INFORMATION: "n" represents ambiguous nucleotides
: NAME/KEY: misc_feature
: LOCATION: (1)...(2866)
: OTHER INFORMATION: n = A,T,C or G
: US-10-095-139-4

Query Match
Best Local Similarity 45.7%; DB 9; Length 2866;
Matches 585; Conservative 0; Mismatches 665; Indels 29; Gaps 3;

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Oy      561  CACTCCTGTTCTTCTGAGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
Db      808  CCAGTCCATCTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 867
Oy      641  CAGTTTGGCAGGAAGAGCTTCTCTGCAACATGCTGTACAGACTGTGCTTCACTT 700
Db      868  CAGTTTGGGCGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 927
Oy      701  CTTGCAATTTTCTCCATCACTGAGAGATTTCACTGTGTATTTGTATCTGTG----- 756
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Db 680 GTGGAGATGCTCTGGAGCCATGCTGTGGCTACCTGCGGACAGGCTGGCGCGG 739  
Qy 657 AACGTTCTCTGCGACCATGGCTGTACAGACTGGCTTCAGCTTCTCTGCAATTTTCTCC 716  
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Search completed: July 5, 2003, 09:00:51  
Job time : 357 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 06:39:30 ; Search time 4827 Seconds

(Without alignments)  
11120.616 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 24791104 segs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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#### SUMMARIES

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| 1          | 2135   | 100.0       | 2135   | 1 PCT-US02-17456-17    | Sequence 17, Appl |
| 2          | 2135   | 100.0       | 2135   | 19 US-09-521-195-2     | Sequence 2, Appl  |
| 3          | 2135   | 100.0       | 2135   | 19 US-09-521-195B-2    | Sequence 2, Appl  |
| 4          | 2135   | 100.0       | 2135   | 66 US-60-226-176-1989  | Sequence 1989, Ap |
| 5          | 2135   | 100.0       | 2135   | 67 US-60-233-468-1989  | Sequence 1989, Ap |
| 6          | 2135   | 100.0       | 2135   | 75 US-60-313-371-1989  | Sequence 1989, Ap |
| 7          | 2135   | 100.0       | 2224   | 61 US-60-172-373-5723  | Sequence 5723, Ap |
| 8          | 2131.8 | 99.9        | 2224   | 65 US-60-213-360-3396  | Sequence 3396, Ap |
| 9          | 2131.8 | 99.9        | 2224   | 71 US-60-278-358-6685  | Sequence 6685, Ap |
| 10         | 2131.8 | 99.9        | 2224   | 76 US-60-324-185-10739 | Sequence 10739, A |
| 11         | 2130.2 | 99.8        | 2135   | 1 PCT-US02-17456-16    | Sequence 16, Appl |
| 12         | 2130.2 | 99.8        | 2135   | 1 PCT-US02-17456-18    | Sequence 18, Appl |
| 13         | 2119.2 | 99.3        | 2137   | 69 US-60-258-325-536   | Sequence 536, App |
| 14         | 1736   | 81.3        | 1736   | 1 PCT-US02-17456-19    | Sequence 19, Appl |
| 15         | 1656   | 77.6        | 1656   | 66 US-60-226-176-1990  | Sequence 1990, Ap |
| 16         | 1656   | 77.6        | 1656   | 67 US-60-233-468-1990  | Sequence 1990, Ap |
| 17         | 1656   | 77.6        | 1656   | 75 US-60-313-371-1990  | Sequence 1990, Ap |
| 18         | 1310.6 | 61.4        | 2080   | 80 US-60-360-207-9909  | Sequence 9909, Ap |
| 19         | 1310.6 | 61.4        | 2083   | 19 US-09-521-195-23    | Sequence 23, Appl |
| 20         | 1310.6 | 61.4        | 2083   | 19 US-09-521-195B-23   | Sequence 23, Appl |
| 21         | 1066.4 | 49.9        | 1831   | 1 PCT-US02-17382-87    | Sequence 87, Appl |

22 1066.4 49.9 1831 1 PCT-US02-17456-21 Sequence 21, Appl  
23 1066.4 49.9 1831 19 US-09-521-195-4 Sequence 4, Appl  
24 1066.4 49.9 1831 19 US-09-521-195-4 Sequence 4, Appl  
25 1066.4 49.9 1831 30 US-09-798-743-2 Sequence 2, Appl  
26 1066.4 49.9 1831 30 US-09-798-743-2 Sequence 2, Appl  
27 1066.4 49.9 1831 66 US-60-226-176-1993 Sequence 193, Ap  
28 1066.4 49.9 1831 66 US-60-226-176-1993 Sequence 193, Ap  
29 1066.4 49.9 1831 67 US-60-226-176-1996 Sequence 193, Ap  
30 1066.4 49.9 1831 67 US-60-226-176-1996 Sequence 193, Ap  
31 1066.4 49.9 1831 75 US-60-233-468-1996 Sequence 193, Ap  
32 1066.4 49.9 1831 75 US-60-233-468-1996 Sequence 193, Ap  
33 1066.4 49.9 1831 75 US-60-313-371-1996 Sequence 193, Ap  
34 1066.4 49.9 1831 75 US-60-313-371-1996 Sequence 193, Ap  
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36 1066.4 49.9 1831 75 US-60-313-371-1996 Sequence 193, Ap  
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43 1066.4 49.9 1831 75 US-60-313-371-1996 Sequence 193, Ap  
44 1066.4 49.9 1831 75 US-60-313-371-1996 Sequence 193, Ap  
45 1066.4 49.9 1831 75 US-60-313-371-1996 Sequence 193, Ap

## ALIGNMENTS

RESULT 1  
PCT-US02-17456-17  
Sequence 17, Application PC/TUS0217456  
GENERAL INFORMATION:  
APPLICANT: EXELTIS, INC.  
FILE OF INVENTION: SLIC22as AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
TITLE REFERENCE: EX02-086C-PC  
CURRENT APPLICATION NUMBER: PCT/US02/17456  
CURRENT FILING DATE: 2002-06-03  
PRIOR APPLICATION NUMBER: US 60/296,076  
PRIOR FILING DATE: 2001-06-05  
PRIOR APPLICATION NUMBER: US 60/328,605  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/357,253  
PRIOR FILING DATE: 2002-02-15  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 2135  
TYPE: DNA  
ORGANISM: Homo sapiens  
PCT-US02-17456-17

Query Match 100.0%; Score 2135; DB 1; Length 2135;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCGGCTCGGCGCCCAATTTCTAAGCGCTGCTCCCGGGGAGCGTTCTAATC 60  
Db 1 CCCCGGCTCGGCGCCCAATTTCTAAGCGCTGCTCCCGGGGAGCGTTCTAATC 60  
QY 61 CTTGGGAGCGCCCGAGCTACAGACAGCTGCTGAGAAAGCTGTCATACCCGATG 120  
Db 61 CTTGGGAGCGCCCGAGCTACAGACAGCTGCTGAGAAAGCTGTCATACCCGATG 120  
QY 121 CAAGTTTGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
Db 121 CAAGTTTGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
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Db 181 GCGAGTGGGCGGCTTCCAGGCGCTCATCTTCTCTCAAGCGCCAGCATATCCCA 240  
QY 241 ATGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300

Db 241 ATGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
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Db 301 TCCCGGAGCGCGGAG 360  
QY 361 TCCCGGAGCGCGGAG 420  
Db 361 TCCCGGAGCGCGGAG 420  
QY 421 TCTCGGCGCTCGGCGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
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QY 481 GCTGCTGAG 540  
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QY 541 GGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
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Db 1021 AGCTGGAAGAT 1080  
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QY 1201 CTTGAGAGAGTGTGAG 1260  
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| Db  | 1321 | TGCGAAGCGTCCAGGCGTTATATCATCTACCTGCAGTACGTCTTCTGGGAGAGAGGTGTGC  | 1380 |
| QY  | 1381 | TTCTCTTCATTCAACCTGGTACCTGTGTGATTTATCTTCTTATCCATTGGTCTGGTCAATGC | 1440 |
| Db  | 1381 | TTCTCTTCATTCAACCTGGTACCTGTGTGATTTATCTTCTTATCCATTGGTCTGGTCAATGC | 1440 |
| QY  | 1441 | TGGGAAAATTTGGGATCACCTCTGTCTTCTTCATGCTGTATGTTCTTACCTGTGAGCTCT   | 1500 |
| Db  | 1441 | TGGGAAAATTTGGGATCACCTCTGTCTTCTTCATGCTGTATGTTCTTACCTGTGAGCTCT   | 1500 |
| QY  | 1501 | ACCCAACCCCTGTAGAGAAATGGCCGGTGGGGGGGCACATCCAGGCGCTCCAGAGTGGGCA  | 1560 |
| Db  | 1501 | ACCCAACCCCTGTAGAGAACTGGCCGGTGGGGGGGCACATCCAGGCGCTCCAGAGTGGGCA  | 1560 |
| QY  | 1561 | GCATCATTTGCCCTTACTTTGTATTACCTCGGTGCTTCAACACAGAACTCTGCCCTACATCG | 1620 |
| Db  | 1561 | GCATCATTTGCCCTTACTTTGTATTACCTCGGTGCTTCAACACAGAACTCTGCCCTACATCG | 1620 |
| QY  | 1621 | TCATGGGTAGTCTGACCTGTCTGTATTTGGAATCTTACCCCTTTTTCCTCGAAAAGTTTG   | 1680 |
| Db  | 1621 | TCATGGGTAGTCTGACCTGTCTGTATTTGGAATCTTACCCCTTTTTCCTCGAAAAGTTTG   | 1680 |
| QY  | 1681 | GAATGACTCTTCCAGAAACCTTTAGACAGATGCAGAAAGTGAATTGGTTCAGATCTGGGA   | 1740 |
| Db  | 1681 | GAATGACTCTTCCAGAAACCTTTAGACAGATGCAGAAAGTGAATTGGTTCAGATCTGGGA   | 1740 |
| QY  | 1741 | AAAAAACAGAGACTCAATGAGAGACAGAGAAATCCCAAGGCTCTAATAACGTCATTTCT    | 1800 |
| Db  | 1741 | AAAAAACAGAGACTCAATGAGAGACAGAGAAATCCCAAGGCTCTAATAACGTCATTTCT    | 1800 |
| QY  | 1801 | GAATAAATATCTACCCCTATTGGTGAAGTGAATAACAGAAATAATAGACCCCTGTGAGAA   | 1860 |
| Db  | 1801 | GAATAAATATCTACCCCTATTGGTGAAGTGAATAACAGAAATAATAGACCCCTGTGAGAA   | 1860 |
| QY  | 1861 | ATTGCTGTCCCACTCAATATGACCTACGTCTACATGCATTTGACACCAAAATGACCTTGCT  | 1920 |
| Db  | 1861 | ATTGCTGTCCCACTCAATATGACCTACGTCTACATGCATTTGACACCAAAATGACCTTGCT  | 1920 |
| QY  | 1921 | ATCAAGAAATGCTCTGATACAGTAAACTCTGATGATTTCTTCAGATTAATGTCTTGCT     | 1980 |
| Db  | 1921 | ATCAAGAAATGCTCTGATACAGTAAACTCTGATGATTTCTTCAGATTAATGTCTTGCT     | 1980 |
| QY  | 1981 | TTACAAACCAACCATTTTCTAGAGAGTCTCTTACTCATTTAATTCGAATGAATGGATTGGT  | 2040 |
| Db  | 1981 | TTACAAACCAACCATTTTCTAGAGAGTCTCTTACTCATTTAATTCGAATGAATGGATTGGT  | 2040 |
| QY  | 2041 | AAGATGCTCTGAAACACTGTTTAGCAGAGACTGTTAAATATCATATTAAGATTACACTC    | 2100 |
| Db  | 2041 | AAGATGCTCTGAAACACTGTTTAGCAGAGACTGTTAAATATCATATTAAGATTACACTC    | 2100 |
| QY  | 2101 | ATTTCGATCATCAATAATCTATCTCAATATTAATAAT                          | 2135 |
| Db  | 2101 | ATTTCGATCATCAATAATCTATCTCAATATTAATAAT                          | 2135 |
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| US-09-521-195-2                             |      |  |      |
| Sequence 2, Application US/09521195         |      |  |      |
| GENERAL INFORMATION:                        |      |  |      |
| : APPLICANT: Nezu, Jun-Ichi                 |      |  |      |
| : APPLICANT: Oku, Asuka                     |      |  |      |
| : TITLE OF INVENTION: TRANSPORTER GENES     |      |  |      |
| : FILE REFERENCE: 06501-057001              |      |  |      |
| : CURRENT APPLICATION NUMBER: US/09/521,195 |      |  |      |
| : PRIOR FILING DATE: 2000-03-07             |      |  |      |
| : PRIOR APPLICATION NUMBER: JP 10/156660    |      |  |      |
| : PRIOR FILING DATE: 1998-05-20             |      |  |      |
| : PRIOR APPLICATION NUMBER: JP 9/260972     |      |  |      |
| : PRIOR FILING DATE: 1997-09-08             |      |  |      |
| : PRIOR APPLICATION NUMBER: PCT/JP98/04009  |      |  |      |
| : PRIOR FILING DATE: 1998-09-07             |      |  |      |
| : NUMBER OF SEQ ID NOS: 32                  |      |  |      |
| : SEQ ID NO 2                               |      |  |      |

[illegible]

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Qy 961 CGCTGTGGTGTATTCTCTGATCTCCCGATGCTGATATCCAGAGAAATTAGAG 1020  
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Db 1021 AGGCTGAAGATATCATCCAAAAGCTGCAAAATGAAACACAGAGCTGTACGAGTGA 1080  
Qy 1081 TATTGATTTCTGTGGAGAGCTAAATCCCTGAAAGCAGAGAAAGCTTTTCATTCTGACC 1140  
Db 1081 TATTGATTTCTGTGGAGAGCTAAATCCCTGAAAGCAGAGAAAGCTTTTCATTCTGACC 1140  
Qy 1141 TGTTCAGAGCTCGGAAATATGCGCATATGACATTAATGCTTGTCTGATGATGCTGA 1200  
Db 1141 TGTTCAGAGCTCGGAAATATGCGCATATGACATTAATGCTTGTCTGATGATGCTGA 1200  
Qy 1201 CCTCAGTGGTATTCTTGTCTGTCTGTGATGCTCCTAATTTACATGAGATGCTTACC 1260  
Db 1201 CCTCAGTGGTATTCTTGTCTGTCTGTGATGCTCCTAATTTACATGAGATGCTTACC 1260  
Qy 1261 TGAACGTCTTCTCTGTCTGTCTGTGATGCTTCAATTCACATTAACAGCTGCTGTAT 1320  
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Qy 1381 TTCTCTTCATTCACACTGATGCTGATGATTAATTAATTAATTAATTAATTAATTAAT 1440  
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Db 1801 GAAAAAATATCTACCCCATTTTGGTGAAGTAAAAAAGAAAAATAGACCTGTGAGAA 1860  
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Db 1861 ATTCTGTTCCTCCAGTGAATGAGTGAATGATGATGATGATGATGATGATGATGAT 1920  
Qy 1921 ATCAAGAAATGCTGCTATACAGTAAATCTGTGATATTTCTTCAGATATGCTGTGT 1980  
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Db 2041 AAGATGCTTTGAAACATTTTGTGAGAGAGTGTGAAATTAATTAATTAATTAATTAAT 2100  
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Db 2101 ATTTCATATCATCAATATCTATTCATAATTAATTAAT 2135

RESULT 3  
US-09-521-195b-2  
; Sequence 2, Application US/09521195B  
; GENERAL INFORMATION:  
; APPLICANT: Nezu, Jun-ichi  
; APPLICANT: Oku, Asuka  
; TITLE OF INVENTION: TRANSPORTER GENES  
; FILE REFERENCE: 06501-057001  
; CURRENT APPLICATION NUMBER: US/09/521,195B  
; CURRENT FILING DATE: 2000-03-07  
; PRIOR APPLICATION NUMBER: JP 10/156660  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: JP 9/260972  
; PRIOR FILING DATE: 1997-09-08  
; PRIOR APPLICATION NUMBER: PCT/JP98/04009  
; PRIOR FILING DATE: 1998-09-07  
; NUMBER OF SEQ ID NOS: 33  
; SEQ ID NO 2  
; LENGTH: 2135  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (147)..(1799)  
US-09-521-195b-2

Query Match 100.0%; Score 2135; DB 19; length 2135;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTTGGGAGAGCGCCAGCTACAGACACTGTCTGAGAACGCTGTATCACCCGTAAGTG 120  
Db 61 CTTGGGAGAGCGCCAGCTACAGACACTGTCTGAGAACGCTGTATCACCCGTAAGTG 120  
Qy 121 CAAGTTTCGAGCGGAGTGGAGACATGCTGAGAACGCTGTATCACCCGTAAGTG 180  
Db 121 CAAGTTTCGAGCGGAGTGGAGACATGCTGAGAACGCTGTATCACCCGTAAGTG 180  
Qy 181 GCGAGTGGGCGCCCTTCCAGCGCTCATCTTCTCTCTACAGCCGACATCATCCCA 240  
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Qy 241 ATGGCTCAATGATATGTCAGTGTGCTGCTGGGAGACCCGAGAGACAGCGTGTGAG 300  
Db 241 ATGGCTCAATGATATGTCAGTGTGCTGCTGGGAGACCCGAGAGACAGCGTGTGAG 300  
Qy 301 TGCAGGAGCGCCGGAACCTGAGCAGCGCTGCGCAACAGATGTCCGCTGCGGCTGC 360  
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Qy 361 GGGAGCGCGCGAGTGTCCCAACAGCTGACGCGCTACCGGCTGCGCACATCCCACT 420  
Db 361 GGGAGCGCGCGAGTGTCCCAACAGCTGACGCGCTACCGGCTGCGCACATCCCACT 420  
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Db 541 GGAATCTGGTGTGAGAGACACTGGAAGTGGCCCTCACCACCTCCCTGTTCTGTAG 600
QY 601 GCGTGTCTCGGCTCCTCTGTCGTGGGAGAGTGCACAGAGTGTGGCAGAGAAAG 660
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    |||
Db 1621 TCATGGAGTGTGACTGTCTCTGATTTGAATCTTACCCCTTTTTCCTGAAAGTTGG 1680
QY 1681 GAATGACTTCCGAAACCTTGAAGCAGATGCAAGAAATGATGTCATGATCGGA 1740
    |||
Db 1681 GAATGACTTCCGAAACCTTGAAGCAGATGCAAGAAATGATGTCATGATCGGA 1740
QY 1741 AAAAACAAGAGACTCAATGAGACAGAGAAATCCCAAGTTCATTAATGCTCATCT 1800
    |||
Db 1741 AAAAACAAGAGACTCAATGAGACAGAGAAATCCCAAGTTCATTAATGCTCATCT 1800
QY 1801 GAAAAAATATCTACCCCAATTTGTGTGAAGTGAAGAAACAGAAATTAAGCCTGTGAGAA 1860
    |||
Db 1801 GAAAAAATATCTACCCCAATTTGTGTGAAGTGAAGAAACAGAAATTAAGCCTGTGAGAA 1860
QY 1861 ATTGCTGTCCCATGAAATGAGACTGACCTGATTAACGATTAACCAAAATGACCTGCT 1920
    |||
Db 1861 ATTGCTGTCCCATGAAATGAGACTGACCTGATTAACGATTAACCAAAATGACCTGCT 1920
QY 1921 ATCAAGAAATGCTCTCATACAGTAAACTGTGATGATTTCTCCAGATTAATGCTTGTCT 1980
    |||
Db 1921 ATCAAGAAATGCTCTCATACAGTAAACTGTGATGATTTCTCCAGATTAATGCTTGTCT 1980
QY 1981 TTCAACAACCAACATTTCTAGAGACTGCTTACTCATTAATTAAGAAATGATGCT 2040
    |||
Db 1981 TTCAACAACCAACATTTCTAGAGACTGCTTACTCATTAATTAAGAAATGATGCT 2040
QY 2041 AAGATGCTTGAACATGTTAGTCAAGAGCTGGTAAATATCATTAAGATTAACACTC 2100
    |||
Db 2041 AAGATGCTTGAACATGTTAGTCAAGAGCTGGTAAATATCATTAAGATTAACACTC 2100
QY 2101 ATTTCATTCATACAAATACTATCCAAATTAAT 2135
    |||
Db 2101 ATTTCATTCATACAAATACTATCCAAATTAAT 2135

RESULT 4
US-60-226-176-1989
; Sequence 1989, Application US/60226176
; GENERAL INFORMATION:
; APPLICANT: Ring, Huijun Z.
; APPLICANT: Malsen, Gareth
; APPLICANT: Townley, David
; APPLICANT: Morris, Macdonald
; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes
; FILE REFERENCE: GX-0013-1 P
; CURRENT APPLICATION NUMBER: US/60/226,176
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2447
; SOFTWARE: PERL Program
; SEQ ID NO 1989
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: GB:AB007448
US-60-226-176-1989

Query Match 100.0%; Score 2135; DB 66; Length 2135;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCGGCTTCGGGCGCCCAATTTCTAAGAGCCCTGCTGCCCCGGGAAAGTTTAAATC 60
    |||
Db 1 CCCCGGCTTCGGGCGCCCAATTTCTAAGAGCCCTGCTGCCCCGGGAAAGTTTAAATC 60
QY 61 CTTGGGAGCGCCCGAGCTACAGACACTGTCTGAGAAAGCTGTATCAACCCGTAGTGG 120
    |||
```

Db 61 CTTGGGAGGCGCCAGCTACAGACACTGCTCCGAGAACGCTGATCATCCCGTAGTTG 120  
QY 121 CAATTTTCGAGCGGCGAGTGGAGACATGCGGAGACTAGACAGAGTATGCTTCCTG 180  
Db 121 CAAATTTTCGAGCGGCGAGTGGAGACATGCGGAGACTAGACAGAGTATGCTTCCTG 180  
QY 181 GCGAGTGGGCGGCTTCAGCGGCTCATCTTTCTTCCGTCAGGCGGAGCATATCCCA 240  
Db 181 GCGAGTGGGCGGCTTCAGCGGCTCATCTTTCTTCCGTCAGGCGGAGCATATCCCA 240  
QY 241 ATGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
Db 241 ATGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
QY 301 TGCGGAGCGCGGCGGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 360  
Db 301 TGCGGAGCGCGGCGGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTG 360  
QY 361 GGGAGCGGCGGAGGTCGCGGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 420  
Db 361 GGGAGCGGCGGAGGTCGCGGAGCGGCTGAGCGGCTGAGCGGCTGAGCGGCTGAG 420  
QY 421 TCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 480  
Db 421 TCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 480  
QY 481 GCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 540  
Db 481 GCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 540  
QY 541 GGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
Db 541 GGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
QY 601 GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
Db 601 GCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
QY 661 TTTCTTCGACACCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 720  
Db 661 TTTCTTCGACACCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 720  
QY 721 GCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 GCTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 TGGAGCTTCATACCTGAGAACGAAATTTCTGGCAAGTCAAGTCAAGTCAAGTCA 840  
Db 781 TGGAGCTTCATACCTGAGAACGAAATTTCTGGCAAGTCAAGTCAAGTCAAGTCA 840  
QY 841 CATTAGAGTGTGACATTTTTCAGTTGGCTATATGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 CATTAGAGTGTGACATTTTTCAGTTGGCTATATGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 TCAATCAGAGTGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 TCAATCAGAGTGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 961 CGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1021 AGGCTGAAGATATCATCCAAAAGCTGCAAAAATGAAACACAGCTGTACCGAGTGA 1080  
Db 1021 AGGCTGAAGATATCATCCAAAAGCTGCAAAAATGAAACACAGCTGTACCGAGTGA 1080  
QY 1081 TATTTGATTTCTGAGAGAGCTAAATCCCTGAAGACAGAAAGCTTTTCAATTCGAGCC 1140  
Db 1081 TATTTGATTTCTGAGAGAGCTAAATCCCTGAAGACAGAAAGCTTTTCAATTCGAGCC 1140  
QY 1141 TGTTCAGAGCTCGGAATATGCAATATGCAATATGCTGCTGCTGCTGCTGCTGCTG 1200  
Db 1141 TGTTCAGAGCTCGGAATATGCAATATGCAATATGCTGCTGCTGCTGCTGCTGCTG 1200

QY 1201 CCTCAGTGGGTTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
Db 1201 CCTCAGTGGGTTACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
QY 1261 TGAACGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
Db 1261 TGAACGTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
QY 1321 TGCAGACGCTGCCAGGCGTTATATCATAGCTGACATGCTGCTGCTGCTGCTGCTG 1380  
Db 1321 TGCAGACGCTGCCAGGCGTTATATCATAGCTGACATGCTGCTGCTGCTGCTGCTG 1380  
QY 1381 TTTCTTCATTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
Db 1381 TTTCTTCATTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
QY 1441 TGGGAAAATTTGGGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
Db 1441 TGGGAAAATTTGGGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500  
QY 1501 ACCCAACCTGCTGACAGAACATGCGGCTGCGGCTGACATCCAGGCTTCAGAGT 1560  
Db 1501 ACCCAACCTGCTGACAGAACATGCGGCTGCGGCTGACATCCAGGCTTCAGAGT 1560  
QY 1561 GATCATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
Db 1561 GATCATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
QY 1621 TCATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
Db 1621 TCATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680  
QY 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGACAGAAAGTGAATGCTGAGATCTG 1740  
Db 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGACAGAAAGTGAATGCTGAGATCTG 1740  
QY 1741 AAAAAAAGAGACTCAATGAGACAGAAAGAAATCCCAAGTCTTAACTGATCTCT 1800  
Db 1741 AAAAAAAGAGACTCAATGAGACAGAAAGAAATCCCAAGTCTTAACTGATCTCT 1800  
QY 1801 GAAAAAATATCTACCCCATTTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860  
Db 1801 GAAAAAATATCTACCCCATTTGCTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1860  
QY 1861 ATTGCTGTTCCCATGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1920  
Db 1861 ATTGCTGTTCCCATGAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1920  
QY 1921 ATCAAGAAATGCTGCTGATACATGAAATGAGTGAAGTGAAGTGAAGTGAAGTGA 1980  
Db 1921 ATCAAGAAATGCTGCTGATACATGAAATGAGTGAAGTGAAGTGAAGTGAAGTGA 1980  
QY 1981 TTACAAACACCATTTTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
Db 1981 TTACAAACACCATTTTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040  
QY 2041 AAGATGCTTGAAGAAATGTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2100  
Db 2041 AAGATGCTTGAAGAAATGTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2100  
QY 2101 ATTTCAAATCATACAAATATATCCAAATTAATAT 2135  
Db 2101 ATTTCAAATCATACAAATATATCCAAATTAATAT 2135

RESULT 5  
US-60-233-468-1989  
; Sequence 1989, Application us/60233468  
; GENERAL INFORMATION:  
; APPLICANT: Ring, Huijun Z.  
; APPLICANT: Malsen, Gareth  
; APPLICANT: Townley, David





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QY 1501 ACCCAACCTGGTACGAGAACATGAGGGGTGACATCCACGAGCTCCAGAGGGGCA 1560
    |||||||
Db 1501 ACCCAACCTGGTACGAGAACATGAGGGGTGACATCCACGAGCTCCAGAGGGGCA 1560
QY 1561 GCATCATGTCGCCCTTACTTTGTTTACCTCGGTGCTTACACAGAAATGCTGCCATCATCG 1620
    |||||||
Db 1561 GCATCATGTCGCCCTTACTTTGTTTACCTCGGTGCTTACACAGAAATGCTGCCATCATCG 1620
QY 1621 TCATGGGTAGTGTGCTGCTGCTGATTTGGAATTCCTACCTTTTTCCTGAAATTTGG 1680
    |||||||
Db 1621 TCATGGGTAGTGTGCTGCTGCTGATTTGGAATTCCTACCTTTTTCCTGAAATTTGG 1680
QY 1681 GAATGACTCTTCCAAACAACTTACGAGAGATGCAAGAAAGTGAATGTTTCAGATTTGGGA 1740
    |||||||
Db 1681 GAATGACTCTTCCAAACAACTTACGAGAGATGCAAGAAAGTGAATGTTTCAGATTTGGGA 1740
QY 1741 AAAAAACAAGAGACTTCATGAGACAGAAAGAAATCCCAAGSTTCTAATTAATGCTATTCCT 1800
    |||||||
Db 1741 AAAAAACAAGAGACTTCATGAGACAGAAAGAAATCCCAAGSTTCTAATTAATGCTATTCCT 1800
QY 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCTGTGAGAGA 1860
    |||||||
Db 1801 GAAAAAATATCTACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCTGTGAGAGA 1860
QY 1861 ATTCGTTGTTCCCACTGAANTGAGACTGATAGCATTTGACACCAAAATGAACTTGGCT 1920
    |||||||
Db 1861 ATTCGTTGTTCCCACTGAANTGAGACTGATAGCATTTGACACCAAAATGAACTTGGCT 1920
QY 1921 ATCAAGAAATGCTGCTGATACAGTAAACTCTGATGATTTCTTCAGATTAATGCTTGGCT 1980
    |||||||
Db 1921 ATCAAGAAATGCTGCTGATACAGTAAACTCTGATGATTTCTTCAGATTAATGCTTGGCT 1980
QY 1981 TTACAAGCAACCATTTCTAGAGAGCTCTTACTCATTAATTAATGAAATGAGATGGT 2040
    |||||||
Db 1981 TTACAAGCAACCATTTCTAGAGAGCTCTTACTCATTAATTAATGAAATGAGATGGT 2040
QY 2041 AAGATGCTTTGAAACATGTTAGTCAAGGACTGTGTAATATACATATAAGATTAACACTC 2100
    |||||||
Db 2041 AAGATGCTTTGAAACATGTTAGTCAAGGACTGTGTAATATACATATAAGATTAACACTC 2100
QY 2101 ATTTCCAATCATACAAATCTATCCCAATTAATAAT 2135
    |||||||
Db 2101 ATTTCCAATCATACAAATCTATCCCAATTAATAAT 2135

RESULT 7
; Sequence 5723, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Deep, Dinsh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ. ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 5723
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 336027.6
US-60-172-373-5723

Query Match 100.0%; Score 2135; DB 61; Length 2224;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCCAGCTGCGCCCAATTTCTACAGCCTGCTGTCCCGGGGAAGCTTTAAATC 60
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Db 56 CCCCAGCTGCGCCCAATTTCTACAGCCTGCTGTCCCGGGGAAGCTTTAAATC 115
QY 61 CTTGGGAGAGGCCCTTACAGACACTCTCTGAGAAAGGTGTATATACCCGTAGTGG 120
    |||||||
Db 116 CTTGGGAGAGGCCCTTACAGACACTCTCTGAGAAAGGTGTATATACCCGTAGTGG 175
QY 121 CAAGTTTCGGAGCGGAGTGGGAAGATGCGGAGCTACGAGAGATGATGCCCTTCCTGG 180
    |||||||
Db 176 CAAGTTTCGGAGCGGAGTGGGAAGATGCGGAGCTACGAGAGATGATGCCCTTCCTGG 235
QY 181 GCGAGTGGGGGCCCTTCCAGCGCTCAATCTTCTCTGTCAGCGCCAGCATATCCCA 240
    |||||||
Db 236 GCGAGTGGGGGCCCTTCCAGCGCTCAATCTTCTCTGTCAGCGCCAGCATATCCCA 295
QY 241 ATGGCTTCAATGATATGATGCTGTCTGCTGGGAGGAGACCCGGAGACACCGGTGGAG 300
    |||||||
Db 296 ATGGCTTCAATGATATGATGCTGTCTGCTGGGAGGAGACCCGGAGACACCGGTGGAG 355
QY 301 TGCCGAGCGCCGCAACCTGAGACGCGCTGGGCGCAACAACAGTGTCCCGTGGCGCTGC 360
    |||||||
Db 356 TGCCGAGCGCCGCAACCTGAGACGCGCTGGGCGCAACAACAGTGTCCCGTGGCGCTGC 415
QY 361 GGAACGGCGCGAGGTGCCCCACAGCTGACAGCGCTACCGGCTCGCCACATGCAACT 420
    |||||||
Db 416 GGAACGGCGCGAGGTGCCCCACAGCTGACAGCGCTACCGGCTCGCCACATGCAACT 475
QY 421 TCTGGGCTGGGGCTGGAAGCGGGGGGCGGAGCGAGCGAGCTGGGGGAGCTGGAGAGGA 480
    |||||||
Db 476 TCTGGGCTGGGGCTGGAAGCGGGGGGCGGAGCGAGCGAGCTGGGGGAGCTGGAGAGGA 535
QY 481 GCTGCTGATGAGCTGGAGATTACAGCAGAGCGCTACCTGTCACCGCTGCTGACAGT 540
    |||||||
Db 536 GCTGCTGATGAGCTGGAGATTACAGCAGAGCGCTACCTGTCACCGCTGCTGACAGT 595
QY 541 GGAATCTGTGTGAGAGACAATGGAAGGTGCCCTTACCACCTCCCTGTTCTTCTAG 600
    |||||||
Db 596 GGAATCTGTGTGAGAGACAATGGAAGGTGCCCTTACCACCTCCCTGTTCTTCTAG 655
QY 601 GCGTGCCTCTGGGCTCTGCTGTCGCCGGGAGCTGTGAGAGGTTGGGAGGAAGAG 660
    |||||||
Db 656 GCGTGCCTCTGGGCTCTGCTGTCGCCGGGAGCTGTGAGAGGTTGGGAGGAAGAG 715
QY 661 TTCCTTGGCAACATGAGCTGTACAGACTGAGCTTCAGCTTCCCTGATTTTTCATCA 720
    |||||||
Db 716 TTCCTTGGCAACATGAGCTGTACAGACTGAGCTTCAGCTTCCCTGATTTTTCATCA 775
QY 721 GCTGGAGATGTTCACTGTATTGTCATGCTGAGGAGTGGGCAAGTCTCCAACTATG 780
    |||||||
Db 776 GCTGGAGATGTTCACTGTATTGTCATGCTGAGGAGTGGGCAAGTCTCCAACTATG 835
QY 781 TGCTAGCTTCAATAGAGACAGAAATCTGGCAGTGCATTTATTTATTTCTCTA 840
    |||||||
Db 836 TGCTAGCTTCAATAGAGACAGAAATCTGGCAGTGCATTTATTTATTTCTCTA 895
QY 841 CATTAGAGATGACATTTTTCAGAGTGGCTATATGCTGCTGCACTGTTTCTTACT 900
    |||||||
Db 896 CATTAGAGATGACATTTTTCAGAGTGGCTATATGCTGCTGCACTGTTTCTTACT 955
QY 901 TCATAGAGACTGCGGAGTCTGCTGTCGGGCTGACGCGTCCCGGAGTGTGTGTCC 960
    |||||||
Db 956 TCATAGAGACTGCGGAGTCTGCTGTCGGGCTGACGCGTCCCGGAGTGTGTGTCC 1015
QY 961 GCGTGTGGGTGTTCTGCTGATGTCGCCGATGGGCTGATATCCAGAGAGATTAGAG 1020
    |||||||
Db 1016 GCGTGTGGGTGTTCTGCTGATGTCGCCGATGGGCTGATATCCAGAGAGATTAGAG 1075
QY 1021 AGGCTGAAGATATATCCAAAAAGCTGCAAAAATGACACACAGCTGTACACAGTGA 1080
    |||||||
Db 1076 AGGCTGAAGATATATCCAAAAAGCTGCAAAAATGACACACAGCTGTACACAGTGA 1135
QY 1081 TATTGATTTCTGTGAGAGACTAAATCCCTGAGAGCAGACAAAGCTTTCAITCTGGACC 1140
    |||||||

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Db 1136 TATTGATCTGTGGAGAGCTAAATCCCTGAAAGAGAGAAAGTTTCATTCTGGACC 1195
QY 1141 TGTTCAGGACTGGGAATTTGGCATATATACCATTTATGCTTTGCTGCTATGAGTGTGA 1200
Db 1196 TGTTCAGGACTGGGAATTTGGCATATATACCATTTATGCTTTGCTGCTATGAGTGTGA 1255
QY 1201 CCTCAGTGGGTACTTGTCTGTCTGTGATGCTCTCAATTTACATGGAGATGGCTTACC 1260
Db 1256 CCTCAGTGGGTACTTGTCTGTCTGTGATGCTCTCAATTTACATGGAGATGGCTTACC 1315
QY 1261 TGACCTGTTTCTCTGTCTGTGATGAAATTCACAGCTTACATTCACAGCTTGTCTAT 1320
Db 1316 TGACCTGTTTCTCTGTCTGTGATGAAATTCACAGCTTACATTCACAGCTTGTCTAT 1375
QY 1321 TGGGAACGCTGGCCAGGCTTATATCATATGCTGACGCTACTGCTTGGGAGAGAGTGTGC 1380
Db 1376 TGGGAACGCTGGCCAGGCTTATATCATATGCTGACGCTACTGCTTGGGAGAGAGTGTGC 1435
QY 1381 TTCTCTTCATTCACATGCTACCTGTGATTTACTTCTTATTCATTTGGTGTGCTATGC 1440
Db 1436 TTCTCTTCATTCACATGCTACCTGTGATTTACTTCTTATTCATTTGGTGTGCTATGC 1495
QY 1441 TGGGAAAAATTTGGGATTCACCTCTCTTCTCCATGCTGTATGCTTTCACCTGCTGAGCTCT 1500
Db 1496 TGGGAAAAATTTGGGATTCACCTCTCTTCTCCATGCTGTATGCTTTCACCTGCTGAGCTCT 1555
QY 1501 ACCCAACCTGGTTCAGAGACATGGGCTGGGGGTGCACATCCAGGCTTCAGAGTGGCA 1560
Db 1556 ACCCAACCTGGTTCAGAGACATGGGCTGGGGGTGCACATCCAGGCTTCAGAGTGGCA 1615
QY 1561 GCATCATTTGCCCTTACTTTGTTTACCTGCTGTTCACAGAAATGCTGCCCTACATCG 1620
Db 1616 GCATCATTTGCCCTTACTTTGTTTACCTGCTGTTCACAGAAATGCTGCCCTACATCG 1675
QY 1621 TCATGGGTAGTCTGACTGCTGATTTGGATCTTACCTTTTTCCTGTAAGATTGG 1680
Db 1676 TCATGGGTAGTCTGACTGCTGATTTGGATCTTACCTTTTTCCTGTAAGATTGG 1735
QY 1681 GAATGACTTTCAGAAACCTTGAAGAGATGACAGAAAGTAAATGTTTCAGATCTGGGA 1740
Db 1736 GAATGACTTTCAGAAACCTTGAAGAGATGACAGAAAGTAAATGTTTCAGATCTGGGA 1795
QY 1741 AAAAAACAAGACATCATGAGAGACAGAAAGAAATCCCAAGTTCTTAATTAATGCTATTC 1800
Db 1796 AAAAAACAAGACATCATGAGAGACAGAAAGAAATCCCAAGTTCTTAATTAATGCTATTC 1855
QY 1801 GAAAAAATATACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGCCCTGTGGAGAA 1860
Db 1856 GAAAAAATATACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGCCCTGTGGAGAA 1915
QY 1861 ATTCGTTGTTCCACTGAATGAGACTGATTAACGATTTGACACCAAAATGAACCTTGT 1920
Db 1916 ATTCGTTGTTCCACTGAATGAGACTGATTAACGATTTGACACCAAAATGAACCTTGT 1975
QY 1921 ATCAAGAAATGCTGCTACATAGTAACTGTGATGATTTCTCCAGATATGCTTGTCT 1980
Db 1976 ATCAAGAAATGCTGCTACATAGTAACTGTGATGATTTCTCCAGATATGCTTGTCT 2035
QY 1981 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTTAATCAATGAAGATGGATGGT 2040
Db 2036 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTTAATCAATGAAGATGGATGGT 2095
QY 2041 AAGATGCTTGAAGAAACATGTTAGTCAAGAGCTGTTAAATATCATATAAAGATTAACATC 2100
Db 2096 AAGATGCTTGAAGAAACATGTTAGTCAAGAGCTGTTAAATATCATATAAAGATTAACATC 2155
QY 2101 ATTTCATCATACAAATATCATATCAATAATAAAT 2135
Db 2156 ATTTCATCATACAAATATCATATCAATAATAAAT 2190

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US-60-213-360-3396
; Sequence 3396, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: EX-0014 P
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL program
; SEQ ID NO: 3396
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Inctyle ID No: 336027.6
US-60-213-360-3396

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Query Match 99.9%; Score 2131.8; DB 65; Length 2224;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCCCCGCTTGGGCCCCCAATTTCTAACAGCCTGCTCTCCCGGGAGACCTTAAACATC 60
Db 56 CCCCCGCTTGGGCCCCCAATTTCTAACAGCCTGCTCTCCCGGGAGACCTTAAACATC 115
QY 61 CTTGGGAGAGCCCCACACTAAGACACTGCTCTGAGAAAGCTGTGATCACCCTGATTTG 120
Db 116 CTTGGGAGAGCCCCACACTAAGACACTGCTCTGAGAAAGCTGTGATCACCCTGATTTG 175
QY 121 CAATTTTCGAGAGCGGAGTGGGAGACATGCGGAGACTAGACAGAGTGATCCCTCTG 180
Db 176 CAATTTTCGAGAGCGGAGTGGGAGACATGCGGAGACTAGACAGAGTGATCCCTCTG 235
QY 181 GCGAGTGGGAGCCCTTCACAGGCTCATCTTCTCGCTCAAGGCGACATCATATCCCA 240
Db 236 GCGAGTGGGAGCCCTTCACAGGCTCATCTTCTCGCTCAAGGCGACATCATATCCCA 295
QY 241 ATGGCTTCAATGTATGTACGTGTTCTCTGCGGGGAGCCCGGAGCAACCGCTGTGAG 300
Db 296 ATGGCTTCAATGTATGTACGTGTTCTCTGCGGGGAGCCCGGAGCAACCGCTGTGAG 355
QY 301 TGGCGAGCGCGGAGACCTGAGCAGCGCTGCGGCAACAATGTTCCGCTGCGCTGC 360
Db 356 TGGCGAGCGCGGAGACCTGAGCAGCGCTGCGGCAACAATGTTCCGCTGCGCTGC 415
QY 361 GGGAGGCGCGAGGTGCCCCACAGCTGACAGCGCTACCGGCTCGCCACATGCGCACT 420
Db 416 GGGAGGCGCGAGGTGCCCCACAGCTGACAGCGCTACCGGCTCGCCACATGCGCACT 475
QY 421 TCTCGCGCTGCGGCTGGAAGCCGCGGCGAGCTGAGACCTGGGCGAGCTGGAAGAGA 480
Db 476 TCTCGCGCTGCGGCTGGAAGCCGCGGCGAGCTGAGACCTGGGCGAGCTGGAAGAGA 535
QY 481 GCTGCTGATGAGCTGGAGTTAGCCAGAGAGTCTAATCTGTACACCTGCTGACGAGT 540
Db 536 GCTGCTGATGAGCTGGAGTTAGCCAGAGAGTCTAATCTGTACACCTGCTGACGAGT 595
QY 541 GGAATCTGAGTGTGAGCAACTGGAAGGTGCCCCCTACAGCTGCCCTGTTCTGTGATG 600
Db 596 GGAATCTGAGTGTGAGCAACTGGAAGGTGCCCCCTACAGCTGCCCTGTTCTGTGATG 655
QY 601 GCGTGTCTCTGCGCTCTCTGTGTGTCGCGGACACTGTACAGAGGTTTGGCAGGAAGAG 660
Db 656 GCGTGTCTCTGCGCTCTCTGTGTGTCGCGGACACTGTACAGAGGTTTGGCAGGAAGAG 715
QY 661 TTCTCTTCCCAACATGCGCTGTACAGACTGCGCTTACGCTTCTGCAAGATTTTCTCATCA 720

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Db 716 TTCTCTGGCAACCATGGCTTACAGACTGGCTTCCTGAGATTTTCTCCATCA 775

QY 721 GCTGGAGATGTTCACTGTTATTTGTCATGCTGGGATGGCCAGATCTCAACTATG 780

Db 776 GCTGGAGATGTTCACTGTTATTTGTCATGCTGGGATGGCCAGATCTCAACTATG 835

QY 781 TGGTACCTTCTACTAGAACAGAAATTTGGCAAGTCAGTTGATATATTTCTCTA 840

Db 836 TGGTACCTTCTACTAGAACAGAAATTTGGCAAGTCAGTTGATATATTTCTCTA 895

QY 841 CATTTGAGATGTCACATTTTGGATGTCATATCTGTCGCACTGTTGTTACT 900

Db 896 CATTTGAGATGTCACATTTTGGATGTCATATCTGTCGCACTGTTGTTACT 955

QY 901 TCATCAGAGACTGGCGAGTGTCTGTGCGCTGACGAGTGGGAGTGTCTGTGTC 960

Db 956 TCATCAGAGACTGGCGAGTGTCTGTGCGCTGACGAGTGGGAGTGTCTGTGTC 1015

QY 961 CGCTGTGTTGTTCAATCTCTGATCTCCCGATGGCTGATATCCAGAGAAATTTAG 1020

Db 1016 CGCTGTGTTGTTCAATCTCTGATCTCCCGATGGCTGATATCCAGAGAAATTTAG 1075

QY 1021 AGGCTGAGATATCATCCAAAAAGCTGCAAAAAATGAACACAGCTTACCAGAGTGA 1080

Db 1076 AGGCTGAGATATCATCCAAAAAGCTGCAAAAAATGAACACAGCTTACCAGAGTGA 1135

QY 1081 TATTTGATTTCTGTGAGAGAGCTAATCCCTGTAACAGACAGAAAGCTTTCATTCGAGC 1140

Db 1136 TATTTGATTTCTGTGAGAGAGCTAATCCCTGTAACAGACAGAAAGCTTTCATTCGAGC 1195

QY 1141 TGTTCAGACTGCGGAATATGGCAATATGACCATATATGCTGCTATGATGCTGA 1200

Db 1196 TGTTCAGACTGCGGAATATGGCAATATGACCATATATGCTGCTATGATGCTGA 1255

QY 1201 CCTCAGTGGGTACTTGTGCTGTGCTGAGATGCTGCAATTTAATGAGAGTGTCTAC 1260

Db 1256 CCTCAGTGGGTACTTGTGCTGTGCTGAGATGCTGCAATTTAATGAGAGTGTCTAC 1315

QY 1261 TGAAGTGTCTCTCTGCTGCTGATTTGAATTCACGTTACATTCACGCTGGCTGCTAT 1320

Db 1316 TGAAGTGTCTCTCTGCTGCTGATTTGAATTCACGTTACATTCACGCTGGCTGCTAT 1375

QY 1321 TGGCAAGCTGCGGAGGCTTATATCATAGCTGCAGTCTGTTGSGGAGAGGCTGTC 1380

Db 1376 TGGCAAGCTGCGGAGGCTTATATCATAGCTGCAGTCTGTTGSGGAGAGGCTGTC 1435

QY 1381 TTCTCTCATTCATGAGTGAAGTGAATTTACTTCTTATCCATTTGCTGTGTCATGTC 1440

Db 1436 TTCTCTCATTCATGAGTGAAGTGAATTTACTTCTTATCCATTTGCTGTGTCATGTC 1495

QY 1441 TGGGAAAAATTTGGATCACTCTGCTTCTCCATGCTTATGTTCTCACTGCTGAGCTCT 1500

Db 1496 TGGGAAAAATTTGGATCACTCTGCTTCTCCATGCTTATGTTCTCACTGCTGAGCTCT 1555

QY 1501 ACCCAACCTGCTCAGGAACATGCGGTGGGGGTCACATCCAGGCTCCAGAGTGGCA 1560

Db 1556 ACCCAACCTGCTCAGGAACATGCGGTGGGGGTCACATCCAGGCTCCAGAGTGGCA 1615

QY 1561 GCATATTTGCCCCCTACTTTGTTTACCTCGGTGCTTAACAAGATGCTGCCCTACATCG 1620

Db 1616 GCATATTTGCCCCCTACTTTGTTTACCTCGGTGCTTAACAAGATGCTGCCCTACATCG 1675

QY 1621 TCATGGGTAGTCTGACTGTCTGATTTGAATCTTACCTTTTTCCTGAAATTTGG 1680

Db 1676 TCATGGGTAGTCTGACTGTCTGATTTGAATCTTACCTTTTTCCTGAAATTTGG 1735

QY 1681 GAATGACTTCTCAGAAACCTTATAGAGAGATGCAAGAAAGTGAATGTTTCAGATCTGGGA 1740

Db 1736 GAATGACTTCTCAGAAACCTTATAGAGAGATGCAAGAAAGTGAATGTTTCAGATCTGGGA 1795

QY 1741 AAAAAACAAGACTCAATGAGAGACAGAAAGAAATCCCAAGGTCTTAACTGATCTCT 1800

Db 1796 AAAAAACAAGACTCAATGAGAGACAGAAAGAAATCCCAAGGTCTTAACTGATCTCT 1855

QY 1801 GAAAAAATATCTACCCCATTTTGTGAAGTGAAGAAAAACAGAAAAATAGACCTGTGAGAA 1860

Db 1856 GAAAAAATATCTACCCCATTTTGTGAAGTGAAGAAAAACAGAAAAATAGACCTGTGAGAA 1915

QY 1861 ATTGTTGTTCCACGTGAATGACGTGATGTAACGATGACACCAAAATGAACCTTGCT 1920

Db 1916 ATTGTTGTTCCACGTGAATGACGTGATGTAACGATGTAACCAAAATGAACCTTGCT 1975

QY 1921 ATCAAGAAATGCTGCTATACAGTAACCTGATGATGTTCTTCAGATTAATGCTTGCT 1980

Db 1976 ATCAAGAAATGCTGCTATACAGTAACCTGATGATGTTCTTCAGATTAATGCTTGCT 2035

QY 1981 TTCAAAACCAACCATTTCTAGAGAGTCTCCTTACTCTATTAATCAATGAATGATGCT 2040

Db 2036 TTCAAAACCAACCATTTCTAGAGAGTCTCCTTACTCTATTAATCAATGAATGATGCT 2095

QY 2041 AAGATGCTTGAAGAAATGTTAGTCAAGACGTGTAAATATCATATTAAGATTAACACTC 2100

Db 2096 AAGATGCTTGAAGAAATGTTAGTCAAGACGTGTAAATATCATATTAAGATTAACACTC 2155

QY 2101 ATTCCAAATCATCAATTAATTAATCCAAATTAATTAAT 2135

Db 2156 ATTCCAAATCATCAATTAATTAATTAATTAATTAAT 2190

RESULT 9

US-60-278-6685

Sequence 6685, Application US/60278258

GENERAL INFORMATION:

APPLICANT: Morris, Macdonald

APPLICANT: Lal, Preethi

APPLICANT: Diep, Binh

TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using

TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide

FILE REFERENCE: GX-0010-1 P

CURRENT APPLICATION NUMBER: US/60/278, 258

CURRENT FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 17730

SOFTWARE: PERL Program

SEQ ID NO 6685

LENGTH: 2224

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

OTHER INFORMATION: Incyte ID No: 336027, 6

US-60-278-6685

Query Match 99.9%; Score 2131.8; DB 71; Length 2224;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCCGCTTGGCGGCCCAATTTCTAACAGCTGCTGTCCCGGGAACTTCTTAACATC 60

Db 56 CCCCCGCTTGGCGGCCCAATTTCTAACAGCTGCTGTCCCGGGAACTTCTTAACATC 115

QY 61 CTTGGGAGAGGCCCTACCTACAGACACTGCTCTGAGAAAGCTGTATCATCCCGTAGTTG 120

Db 116 CTTGGGAGAGGCCCTACCTACAGACACTGCTCTGAGAAAGCTGTATCATCCCGTAGTTG 175

QY 121 CAATTTTCGAGGCGGAGTGGGAAGCATGGGGGACTGAGAGAGTGAATGCTTCTCTGG 180

Db 176 CAATTTTCGAGGCGGAGTGGGAAGCATGGGGGACTGAGAGAGTGAATGCTTCTCTGG 235

QY 181 GCGAGTGGGGGCCCTTCACAGGCTCATCTTCTCTGCTCAAGCGCCAGCATCATCCCA 240

Db 236 GCGAGTGGGGGCCCTTCACAGGCTCATCTTCTCTGCTCAAGCGCCAGCATCATCCCA 295

QY 241 ATGCTTCAATGATGATGCTGCTGCTGCTGCGGGGAGACCCCGGAGACACCGCTGCGAG 300

Db 296 ATGCTTCAATGATGATGCTGCTGCTGCTGCGGGGAGACCCCGGAGACACCGCTGCGAG 355



NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No: 1398921.3  
US-60-324-185-10739

Query Match 99.98; Score 2131.8; DB 76; Length 2224;  
Best Local Similarity 99.98; Pred. No. 0;  
Matches 2133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCCCAGCTTGGCCGCCCAATTTCTACAGAGCTGCTGCTCCCGGGGAGAGTCTTACATC 60
DB 56 CCCCAGCTTGGCCGCCCAATTTCTACAGAGCTGCTGCTCCCGGGGAGAGTCTTACATC 115
QY 61 CTTGGGAGAGCCGCCAGCTACAGACACTGCTCTGAGAAAGCTGTCATCAGCCGTAATTG 120
DB 116 CTTGGGAGAGCCGCCAGCTACAGACACTGCTCTGAGAAAGCTGTCATCAGCCGTAATTG 175
QY 121 CAAGTTTCGAGAGGCGAGTGGGAGAGATGCGGAGCTACAGACAGAGTGAATGCGCTTCTG 180
DB 176 CAAGTTTCGAGAGGCGAGTGGGAGAGATGCGGAGCTACAGACAGAGTGAATGCGCTTCTG 235
QY 181 GCGAGTGGGGCCCTTCAGAGCGCTCATCTCTTCTGCTCAAGCGCAGATCATCCCA 240
DB 236 GCGAGTGGGGCCCTTCAGAGCGCTCATCTCTTCTGCTCAAGCGCAGATCATCCCA 295
QY 241 ATGGCTTCAATGGTATGTCAGTGTCTTCTGCGGGGGAACCCCGAGACCGCTGTGAG 300
DB 296 ATGGCTTCAATGGTATGTCAGTGTCTTCTGCGGGGGAACCCCGAGACCGCTGTGAG 355
QY 301 TGGCGAGAGCGCGGAGACCTGAGAGCGCTGGGGCAACAAGATGTCGGCTGCGGCTGC 360
DB 356 TGGCGAGAGCGCGGAGACCTGAGAGCGCTGGGGCAACAAGATGTCGGCTGCGGCTGC 415
QY 361 GGGAGGCGCGGAGAGTGGCCCAAGCTGAGCGCTACCGGCTGCGGCAACATGCGCACT 420
DB 416 GGGAGGCGCGGAGAGTGGCCCAAGCTGAGCGCTACCGGCTGCGGCAACATGCGCACT 475
QY 421 TCTCGGCGCTCGGGCTGAGAGCGGGCGCGAGCTGAGACCTGGGGACGTTGGAGCAGAGA 480
DB 476 TCTCGGCGCTCGGGCTGAGAGCGGGCGCGAGCTGAGACCTGGGGACGTTGGAGCAGAGA 535
QY 481 GCTGCTGATGGCTGGGAGTTGAGCAGAGAGCTACCTGTCACACCGTCGACCGAGT 540
DB 536 GCTGCTGATGGCTGGGAGTTGAGCAGAGAGCTACCTGTCACACCGTCGACCGAGT 595
QY 541 GGAATCTGTGTGTGAGAGCAACTGGAAGGTGCCCTCAACAACCTCCCTGTTCTGTAG 600
DB 596 GGAATCTGTGTGTGAGAGCAACTGGAAGGTGCCCTCAACAACCTCCCTGTTCTGTAG 655
QY 601 GCGTGTCTCTGCGGCTCTCTGCTCGGGGAGCTGTACAGACAGGTTGGCAGAGAGACG 660
DB 656 GCGTGTCTCTGCGGCTCTCTGCTCGGGGAGCTGTACAGACAGGTTGGCAGAGAGACG 715
QY 661 TTCTCTTGGCAACCATGGCTGTACAGAGCTGAGCTTCCGCGAGATTTCTCATCA 720
DB 716 TTCTCTTGGCAACCATGGCTGTACAGAGCTGAGCTTCCGCGAGATTTCTCATCA 775
QY 721 GCTGGGAGATGTTCACTGTATTGTTGTCATCGTGGGAGTGGGCCAGATCTCCAACTAG 780
DB 776 GCTGGGAGATGTTCACTGTATTGTTGTCATCGTGGGAGTGGGCCAGATCTCCAACTAG 835
QY 781 TGGTAGCCTTCATACAGAGAGAGAAATCTTGGCAAGTCAGTCTGTATTATTTCTCA 840
DB 836 TGGTAGCCTTCATACAGAGAGAGAAATCTTGGCAAGTCAGTCTGTATTATTTCTCA 895
QY 841 CATTAGAGAGTGTACATTTTTCAGATTGGCTATATGCTGCTGCACTGTTTCTTACT 900
DB 896 CATTAGAGAGTGTACATTTTTCAGATTGGCTATATGCTGCTGCACTGTTTCTTACT 955
QY 901 TCATCAGAGACTGGCGAGTGTCTGTGCGCTGACGCTGCGGGAGTGTCTGTCTCC 960
DB 956 TCATCAGAGACTGGCGAGTGTCTGTGCGCTGACGCGGGAGTGTCTGTCTCC 1015
QY 961 CGCTGTGTGTCTCATTTCCGAACTCTCCCGATGGCTGATATCCGAGAGAGATTTAGAG 1020
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DB 1016 CGCTGTGGAGTTTACTTCTGTGAATCTCCCGCATGGCTGATATCCAGAGAGATTTAGAG 1075
QY 1021 AGGCTGAAGATATCTCCAAAAGCTGCAAAAATGTAACACAGAGCTGTACAGAGTGA 1080
DB 1076 AGGCTGAAGATATCTCCAAAAGCTGCAAAAATGTAACACAGAGCTGTACAGAGTGA 1135
QY 1081 TATTTGATCTGTGAGAGAGCTAAATCCCGTAAGCAGACAGAAAGCTTCAATCGGACC 1140
DB 1136 TATTTGATCTGTGAGAGAGCTAAATCCCGTAAGCAGACAGAAAGCTTCAATCGGACC 1195
QY 1141 TGTTCAGAGACTGGAATATTTGCAATATGACCATATGCTCTTGTGCTATGATGATGTA 1200
DB 1196 TGTTCAGAGACTGGAATATTTGCAATATGACCATATGCTCTTGTGCTATGATGATGTA 1255
QY 1201 CCTCAGTGGGTTACTTCTGCTGTCTGTGAGATGCTCCATTAATTTACATGAGATGCTTACC 1260
DB 1256 CCTCAGTGGGTTACTTCTGCTGTCTGTGAGATGCTCCATTAATTTACATGAGATGCTTACC 1315
QY 1261 TGAACGTGTTCTCTCTGCTGATTTGAATTCACGTTTACATTAACAGCTGGGCTGAT 1320
DB 1316 TGAACGTGTTCTCTCTGCTGATTTGAATTCACGTTTACATTAACAGCTGGGCTGAT 1375
QY 1321 TGGGAAGCTGTGCCAGGCTTATATCATAGCTGACGATGTTGCGGAGAGAGTGTGC 1380
DB 1376 TGGGAAGCTGTGCCAGGCTTATATCATAGCTGACGATGTTGCGGAGAGAGTGTGC 1435
QY 1381 TTCTCTTCAATCACTGATGCTGTGATTTATATTTCTTATCATTTGATGCTGATGCT 1440
DB 1436 TTCTCTTCAATCACTGATGCTGTGATTTATATTTCTTATCATTTGATGCTGATGCT 1495
QY 1441 TGGGAAAATTTGGGATCACTCTGCTTCTCATGCTATAGTCTTCACTGATGCT 1500
DB 1496 TGGGAAAATTTGGGATCACTCTGCTTCTCATGCTATAGTCTTCACTGATGCT 1555
QY 1501 ACCCAACCTGTGTGAGAAACATGGCGGTGGGGGTACATCCAGGCTCCAGAGTGGCA 1560
DB 1556 ACCCAACCTGTGTGAGAAACATGGCGGTGGGGGTACATCCAGGCTCCAGAGTGGCA 1615
QY 1561 GCATGATGCCCCCTACTTGTGTTTCTGCTGCTGCTTAACAAGAAATGCTGCCATACATG 1620
DB 1616 GCATGATGCCCCCTACTTGTGTTTCTGCTGCTGCTTAACAAGAAATGCTGCCATACATG 1675
QY 1621 TCATGGGTAGTCTGCTGCTGCTGATTTGAATCTTACCCCTTTTCCCTGAAAGTTGG 1680
DB 1676 TCATGGGTAGTCTGCTGCTGCTGATTTGAATCTTACCCCTTTTCCCTGAAAGTTGG 1735
QY 1681 GATGACCTTTCAGAAACCTTAGAGCAGATGAGAGAAAGTGAATGTTGATGTGGGA 1740
DB 1736 GATGACCTTTCAGAAACCTTAGAGCAGATGAGAGAAAGTGAATGTTGATGTGGGA 1795
QY 1741 AAAAAACAAGAGACATGAGAGAGAGAGAAATCCCAAGTCTTATTAATCTGATCT 1800
DB 1796 AAAAAACAAGAGACATGAGAGAGAGAGAAATCCCAAGTCTTATTAATCTGATCT 1855
QY 1801 GAAAAAATATCTACCCATTGGTGAAGTGAAGAAACAGAAATTAAGACCTGTGAGAA 1860
DB 1856 GAAAAAATATCTACCCATTGGTGAAGTGAAGAAACAGAAATTAAGACCTGTGAGAA 1915
QY 1861 ATTGTTGTGCTCACTGAAATGAGACTGTAACGATTTGACACCAAAATGAACTGTGCT 1920
DB 1916 ATTGTTGTGCTCACTGAAATGAGACTGTAACGATTTGACACCAAAATGAACTGTGCT 1975
QY 1921 ATCAAGAAATGCTCTCATACAGTAAATCTGAGATGATTTCTCCAGATATATGCTTGTCT 1980
DB 1976 ATCAAGAAATGCTCTCATACAGTAAATCTGAGATGATTTCTCCAGATATATGCTTGTCT 2035
QY 1981 TTACAACCAACCATTTCTAGAGACTCTCTTACTCATTAATTAATGAATGATGGT 2040
DB 2036 TTACAACCAACCATTTCTAGAGAGTCTCTTACTCATTAATTAATGAATGATGGT 2095
QY 2041 AAGATGCTTGAAGAAACATGTTAGTCAAGAGCTGTGAATATCATATAAGATTAACACTC 2100
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Db 2096 AAGATGCTTGAAGAAACGTTAGTCAAGACCTGGTAAATAATACATATATAAGATTAAACATC 2155  
QY 2101 ATTTCATCATATACAAATACTATATCCAAATATAAT 2135  
Db 2156 ATTTCATCATATACAAATACTATATCCAAATATAAT 2190

RESULT 11  
PCT-US02-17456-18  
: Sequence 18, Application PC/TUS0217456  
: GENERAL INFORMATION:  
: APPLICANT: EXELIXIS, INC.  
: TITLE OF INVENTION: SEC22AS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE  
: FILE REFERENCE: EX02-086C-PC  
: CURRENT APPLICATION NUMBER: PCT/US02/17456  
: PRIOR FILING DATE: 2002-06-03  
: PRIOR APPLICATION NUMBER: US 60/296,076  
: PRIOR FILING DATE: 2001-06-05  
: PRIOR APPLICATION NUMBER: US 60/328,605  
: PRIOR FILING DATE: 2001-10-10  
: PRIOR APPLICATION NUMBER: US 60/357,253  
: PRIOR FILING DATE: 2002-02-15  
: NUMBER OF SEQ ID NOS: 42  
: SOFTWARE: PatentIn version 3.1  
: SEQ ID NO 18  
: LENGTH: 2135  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
PCT-US02-17456-18

Query Match 99.8%; Score 2130.2; DB 1; Length 2135;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCGGCTTCGCGCCCAATTTCTAACAGCCTGCTGCCCGGGAACGTTCTTAACATC 60  
Db 1 CCCCGGCTTCGCGCCCAATTTCTAACAGCCTGCTGCCCGGGAACGTTCTTAACATC 60  
QY 61 CTGGGGAGGCGCCCACTACAGACACTCTCTGAGAACGCTGTATCAACCGGTGTTG 120  
Db 61 CTGGGGAGGCGCCCACTACAGACACTCTCTGAGAACGCTGTATCAACCGGTGTTG 120  
QY 121 CAAGTTTCGAGGCGCAGTGGGAAGCATGCGGAGTACAGCAGAGTGTATGCTCTCTG 180  
Db 121 CAAGTTTCGAGGCGCAGTGGGAAGCATGCGGAGTACAGCAGAGTGTATGCTCTCTG 180  
QY 181 GCGAGTGGGCGCTTCAGAGCGCTCATCTTCTCTGCTCAGCGCCAGCATATCCCA 240  
Db 181 GCGAGTGGGCGCTTCAGAGCGCTCATCTTCTCTGCTCAGCGCCAGCATATCCCA 240  
QY 241 ATGACCTTCATATGATGTACGTGCTGTCTTGCGGGGACCCCGGAGCAACCGCTGTGAG 300  
Db 241 ATGACCTTCATATGATGTACGTGCTGTCTTGCGGGGACCCCGGAGCAACCGCTGTGAG 300  
QY 301 TGCAGGAGCGCGGAACTGAGCAGCGCTGAGCAACAAACAGTGTCCGCTGCGCTG 360  
Db 301 TGCAGGAGCGCGGAACTGAGCAGCGCTGAGCAACAAACAGTGTCCGCTGCGCTG 360  
QY 361 GGGAGGCGCGGAGGTGCCCAAGCTGACGCGGTACCGGCTGCGCACCATATGCCAAT 420  
Db 361 GGGAGGCGCGGAGGTGCCCAAGCTGACGCGGTACCGGCTGCGCACCATATGCCAAT 420  
QY 421 TCTCGGCGCTCGGAGTGGAGCCGGGGCGGAGCTGAGACCTGGGGGAGCTGGAGCAGAGA 480  
Db 421 TCTCGGCGCTCGGAGTGGAGCCGGGGCGGAGCTGAGACCTGGGGGAGCTGGAGCAGAGA 480  
QY 481 GCTGCGCTGAGTGGAGTGGAGCTGAGCAGAGCTGACCTGAGCAGCTGAGCAGAGT 540  
Db 481 GCTGCGCTGAGTGGAGTGGAGCTGAGCAGAGCTGACCTGAGCAGCTGAGCAGAGT 540  
QY 541 GGAATCTGCTGTGAGGACAACTGAGAAAGTGGCCCTTCAACCACTCCCTGTTCTGTAG 600  
Db 541 GGAATCTGCTGTGAGGACAACTGAGAAAGTGGCCCTTCAACCACTCCCTGTTCTGTAG 600

QY 601 GCGTGTCTCGGCTCTCTGCTGTCGCGGACCTGTACAGAGGTTTGGCAGGAAGACG 660  
Db 601 GCGTGTCTCGGCTCTCTGCTGTCGCGGACCTGTACAGAGGTTTGGCAGGAAGACG 660  
QY 661 TTCTCTTGGCAACCATGGCTGTACAGACTGGCTTACGCTTCCGCAATTTTCTCATCA 720  
Db 661 TTCTCTTGGCAACCATGGCTGTACAGACTGGCTTACGCTTCCGCAATTTTCTCATCA 720  
QY 721 GCTGGAGATGTTCACTGCTGATTTGTCATCGTGGGATGGGACAGATTCACATATG 780  
Db 721 GCTGGAGATGTTCACTGCTGATTTGTCATCGTGGGATGGGACAGATTCACATATG 780  
QY 781 TGGTAGCCTTCATCTAGAGACAGAAATTTTGGCAATGCTGATTAATTCCTA 840  
Db 781 TGGTAGCCTTCATCTAGAGACAGAAATTTTGGCAATGCTGATTAATTCCTA 840  
QY 841 CATTAGAGTGTGACATTTTGGAGTGGCTATATGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 CATTAGAGTGTGACATTTTGGAGTGGCTATATGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 TCATCAGAGACTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 TCATCAGAGACTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 CGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 961 CGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
QY 1021 AGGCTGAAGATATATCCAAAGCTGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 1080  
Db 1021 AGGCTGAAGATATATCCAAAGCTGCAAAATGCAAAATGCAAAATGCAAAATGCAAA 1080  
QY 1081 TATTGATTTCTGAGAGAGCTAAATCCCTGAGACAGAGAGCTTATTCCTGAGAC 1140  
Db 1081 TATTGATTTCTGAGAGAGCTAAATCCCTGAGACAGAGAGCTTATTCCTGAGAC 1140  
QY 1141 TGTTCAGAGCTGGAATATGCAATATGACATATATGCTGCTGCTGCTGCTGCTG 1200  
Db 1141 TGTTCAGAGCTGGAATATGCAATATGACATATATGCTGCTGCTGCTGCTGCTG 1200  
QY 1201 CCTCAGTGGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
Db 1201 CCTCAGTGGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
QY 1261 TGAACCTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
Db 1261 TGAACCTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320  
QY 1321 TGCAGAGCGCGCGGCTTATATCATAGCTGAGTACTGCTGCTGCTGCTGCTGCTG 1380  
Db 1321 TGCAGAGCGCGCGGCTTATATCATAGCTGAGTACTGCTGCTGCTGCTGCTGCTG 1380  
QY 1381 TTCTCTTCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
Db 1381 TTCTCTTCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440  
QY 1441 TGGGAAATTTGGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Db 1441 TGGGAAATTTGGGATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
QY 1501 ACCCAACCTGCTGAGAACTGAGGCTGAGGCTGACATCCAGCGGCTCCAGAGTGGGCA 1560  
Db 1501 ACCCAACCTGCTGAGAACTGAGGCTGAGGCTGACATCCAGCGGCTCCAGAGTGGGCA 1560  
QY 1561 GCATCATTTGCCCTACTTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
Db 1561 GCATCATTTGCCCTACTTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
QY 1621 TCATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
Db 1621 TCATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680

|    |      |  |      |
|----|------|--|------|
| QY | 1681 | GAAGACTCTTCCGAAAGACCTTGAGAGAGATGCGAAAGTGAATGGTTCAGATCTGGGA       | 1740 |
|    |      |  |      |
| Db | 1681 | GAAGACTCTTCCGAAAGCCTTAAAGAGATGCGAAAGTGAATGGTTCAGATCTGGGA         | 1740 |
| QY | 1741 | AAAAACAGAGACTCATGATGAGAGACAGACAGAAAAATCCCAAGTCTCTATAACTGCATTTCT  | 1800 |
| Db | 1741 | AAAAACAGAGACTCATGATGAGAGACAGAGAAAAATCCCAAGTCTCTATAACTGCATTTCT    | 1800 |
| QY | 1801 | GAAAAAATATCTACCCCATTTGGTGAAGTGAAAAACGAAAAATPAAGCCTGTGGAGAA       | 1860 |
| Db | 1801 | GAAAAAATATCTACCCCATTTGGTGAAGTGAAAAACGAAAAATPAAGCCTGTGGAGAA       | 1860 |
| QY | 1861 | ATTGCTGTTCCCACTGAAATGAGCTGACTTAACGATGTGACACCAAAATGACCTTGCT       | 1920 |
| Db | 1861 | ATTGCTGTTCCCACTGAAATGAGCTGACTTAACGATGTGACACCAAAATGACCTTGCT       | 1920 |
| QY | 1921 | ATCAGAGAAATGCTGCTCATACAGTAAACTGTGATGATTTCTTCAGATATATGTCCTTGCT    | 1980 |
| Db | 1921 | ATCAGAGAAATGCTGCTCATACAGTAAACTGTGATGATTTCTTCAGATATATGTCCTTGCT    | 1980 |
| QY | 1981 | TTACAAACCAACCAATTTCTAGAGAGTCCCTACTCATATTAATCAATGAATGGATGGT       | 2040 |
| Db | 1981 | TTACAAACCAACCAATTTCTAGAGAGTCCCTACTCATATTAATCAATGAATGGATGGT       | 2040 |
| QY | 2041 | AAGATGTCCTTGAAACAACATGTTAGTCAAGAGACTGGTAAATATACATATAAAGATTAACTTC | 2100 |
| Db | 2041 | AAGATGTCCTTGAAACAACATGTTAGTCAAGAGACTGGTAAATATACATATAAAGATTAACTTC | 2100 |
| QY | 2101 | ATTTCGAATCATACAAATACTATCTCCAAATATAAAAT                           | 2135 |
| Db | 2101 | ATTTCGAATCATACAAATACTATCTCCAAATATAAAAT                           | 2135 |

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RESULT 12
PCT-US02-17456-16
; Sequence 16, Application PC/TUS0217456
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: SRC22a AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-086C-PC
; CURRENT APPLICATION NUMBER: PCT/US02/17456
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 2166
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-17456-16

```

|                            |        |               |           |              |
|----------------------------|--------|---------------|-----------|--------------|
| Query Match                | 99.8%  | Score 2130.2; | DB 1;     | Length 2166; |
| Best Local Similarity      | 99.98% | Pred. No. 0;  |           |              |
| Matches 2132; Conservative | 0;     | Mismatches 3; | Indels 0; | Gaps 0       |

QY 1 CCCCAGCTTCGGCCCCCAATTCTTAACAGCTGCTGTGCCCGGGAAAGTTCTTAACATC 60

Db 13 CCCCAGCTTCGGCCCCCAATTCTTAACAGCTGCTGTGCCCGGGAAAGTTCTTAACATC 72

QY 61 CTTGGGAGAGCGCCCCAGCTACAGACACGTGTCCTAGAAAGCTGTGCATCACCCGTAGTTG 120

Db 73 CTTGGGAGAGCGCCCCAGCTACAGACACGTGTCTAGAAAGCTGTGCATCACCCGTAGTTG 132

QY 121 CAAGTTTGGAGCGGACAGTGGGAGACATGCGGAGATAGACAGCGGTGATCGCCTTCCTGG 180

Db 133 CAAGTTTGGAGCGGACAGTGGGAGACATGCGGAGATAGACAGCGGTGATCGCCTTCCTGG 192

QY 181 GCGAGTGGAGGCCCTTTCACAGGCGCTCATCTTCTTCCTGCTAGCGCCACATCATCCCA 240

|    |      |   |      |
|----|------|---|------|
| Db | 193  | GCAGATGGGGCCCTTCCAGCGCCTCATCTTCTTCTGCTACGGCCACGATCATCCCCA       | 252  |
| Qy | 241  | ATGACCTCAAAAGTATGTCACTCGTGTGTTCCATGCGGGGAGACCCCGAGACACCGCTGTGAG | 300  |
| Db | 253  | ATGGCTTCAATAGTATGTCACTCGTGTGTTCCATGCGGGGAGACCCCGAGACACCGCTGTGAG | 312  |
| Qy | 301  | TGCCGAGACGCCGACACCTGACAGCGGCTTGCGCAACACAGTGTCCCGCTGGCGCTGC      | 360  |
| Db | 313  | TGCCGAGACGCCGACACCTGAGACGCGCTGGCCCAACACAGTGTCCCGCTGGCGCTGC      | 372  |
| Qy | 361  | GGGACGGCCCGGAGAGTGGCCCAACGCTGACACCGCTACCGGCTGCGCACCTGCGCACT     | 420  |
| Db | 373  | GGGACGGCCCGGAGAGTGGCCCAACGCTGACACCGCTACCGGCTGCGCACCTGCGCACT     | 432  |
| Qy | 421  | TCTCGGCGCTTGAGGCTGAGAGCCGGGGCGACGTTGAACTTGGGGAGCTGGAGCAGAGA     | 480  |
| Db | 433  | TCTCGGCGCTTGAGGCTGAGAGCCGGGGCGACGTTGAACTTGGGGAGCTGGAGCAGAGA     | 492  |
| Qy | 481  | GCTGCGCTGAGAGCTGGGAGTTTCAGACCAAGACGCTCTACTCTCCACCGCTGTCAGCAGT   | 540  |
| Db | 493  | GCTGCGCTGAGAGCTGGGAGTTTCAGACCAAGACGCTCTACTCTCCACCGCTGTCAGCAGT   | 552  |
| Qy | 541  | GGAACTGTGTGTGAGGAGCAACAGTGGAAAGAGCCCGCTACACACGTCCTGTCTTCGTAG    | 600  |
| Db | 553  | GGAACTGTGTGTGAGGAGCAACAGTGGAAAGAGTCCCGCTACACACCTCCTGTCTTCGTAG   | 612  |
| Qy | 601  | GCGTGCCTCTGGGCTCTTCTGCTGTCGGGGGACGCTGTACAGACGAGTTTGGCAGAGAAACG  | 660  |
| Db | 613  | GCGTGCCTCTGGGCTCTTCTGCTGTCGGGGGACGCTGTACAGACGAGTTTGGCAGAGAAACG  | 672  |
| Qy | 661  | TTCTCTTCGCAACCATGGCTGTACAGACTGCGCTTACAGTTCTCTGACATTTTCTTCATCA   | 720  |
| Db | 673  | TTCTCTTCGCAACCATGGCTGTACAGACTGCGCTTACAGTTCTCTGACATTTTCTTCATCA   | 732  |
| Qy | 721  | GCTGGGAGATGTTCACCTGTGTTATTTGTCATCGGAGGAGTGGGCGAGTCCCAACATAG     | 780  |
| Db | 733  | GCTGGGAGATGTTCACCTGTGTTATTTGTCATCGTGGGATGGGCGAGTCTCCAACTATG     | 792  |
| Qy | 781  | TGCTGAGCCTTCACTACTAGGAACAGAAATCTTGGCACTCAGTTGCTATATATCTCTTA     | 840  |
| Db | 793  | TGCTGAGCCTTCACTACTAGGAACAGAAATCTTGGCACTCAGTTGCTATATATCTCTTA     | 852  |
| Qy | 841  | CATTAGAGAGTGTGCACATTTTTCGACGTGGCTATATCTGCTGCACTGTTTGGTTACT      | 900  |
| Db | 853  | CATTAGAGAGTGTGCACATTTTTCGACGTGGCTATATCTGCTGCACTGTTTGGTTACT      | 912  |
| Qy | 901  | TCATCAGAGACTGGCGGAGTGCCTGCGTGGGCGTGAAGGTGCGGAGATGCGTGTGCC       | 960  |
| Db | 913  | TCATCAGAGACTGGCGGAGTGCCTGCGTGGGCGTGAAGGTGCGGAGATGCGTGTGCC       | 972  |
| Qy | 961  | CGCTGTGGTGGTTCAATTCCTGTAATCCCGCATGGCTATATCCACAGAGAAATTTAGAG     | 1020 |
| Db | 973  | CGCTGTGGTGGTTCAATTCCTGTAATCCCGCATGGCTATATCCACAGAGAAATTTAGAG     | 1032 |
| Qy | 1021 | AGGCTGAAGATATCATCCAAAAAGCTGCAAAAATGACACACAGCTGTACACAGCATGA      | 1080 |
| Db | 1033 | AGGCTGAAGATATCATCCAAAAAGCTGCAAAAATGACACACATAGCTGTACACAGCATGA    | 1092 |
| Qy | 1081 | TATTTGATTTCTGTGAGAGAGCTAAATCCCGCTGAAGACACAGAAAGCTTTCAATCTGAGAC  | 1144 |
| Db | 1093 | TATTTGATTTCTGTGAGAGAGCTAAATCCCGCTGAAGACACAGAAAGCTTTCAATCTGAGAC  | 1156 |
| Qy | 1141 | TGTTTAGGACCTGGAAATATGTCATTAAGACCATATGCTTTCGTGTATGAGATGTGAG      | 1200 |
| Db | 1153 | TGTTTAGGACCTGGAAATATGTCATTAAGACCATATATGCTTTCGTGTATGAGATGTGAG    | 1212 |
| Qy | 1201 | CCTCAGTGGGTACTTTCCTGTCTGTCTGTGATGCTCTAATTTACATGAGAGTGGCTACG     | 1260 |
| Db | 1213 | CCTCAGTGGGTACTTTCCTGTCTGTCTGTGATGCTCTAATTTACATGAGAGTGGCTACG     | 1272 |
| Qy | 1261 | TGAACGTGTTCTCTCTGCTTGAATTTCCAGCTTACATTTACAGCTGGCGCTAT           | 1320 |

|  |      |   |      |
|--|------|---|------|
| Db   | 1273 | TGAACCTGTTTCCTCTCCCTGATGTGAATTCACGCTTAATTAACAGCCTGCGTCTAT     | 1332 |
| Qy   | 1321 | TGCGAACCGCTGCCAGCGGCTTAATATCATATAGCTGCAGTACTGTCTGGGAGAGGTGTGC | 1380 |
| Db   | 1333 | TGCGAACCGCTGCCAGCGGCTTAATATCATATAGCTGCAGTACTGTCTGGGAGAGGTGTGC | 1392 |
| Qy   | 1381 | TTCTCTTATTCATCACTGGTACCTGGAGATTTTAACTCTTATTCATGAGTGTGTGCTATGC | 1440 |
| Db   | 1393 | TTCTCTTATTCATCACTGGTACCTGGAGATTTTAACTCTTATTCATGAGTGTGTGCTATGC | 1452 |
| Qy   | 1441 | TGGGAAATTTTGGGATCACTCTGTCTTCTCCATGCTGTATGCTTACTGCTAGCTCT      | 1500 |
| Db   | 1453 | TGGGAAATTTTGGGATCACTCTGTCTTCTCCATGCTGTATGCTTACTGCTAGCTCT      | 1512 |
| Qy   | 1501 | ACCCAAACCTGTGTAGAGAACATGGCGGTGGGGGTGCACATCCAGCGCTCCAGAGTGGGCA | 1560 |
| Db   | 1513 | ACCCAAACCTGTGTAGAGAACATGGCGGTGGGGGTGCACATCCAGCGCTCCAGAGTGGGCA | 1572 |
| Qy   | 1561 | GCATCATTTGCCCGCTACTTTGTTTAACTCCGCTGCTTACACAGAAATCTGCGCTACATCG | 1620 |
| Db   | 1573 | GCATCATTTGCCCGCTACTTTGTTTAACTCCGCTGCTTACACAGAAATCTGCGCTACATCG | 1632 |
| Qy   | 1621 | TCATGGGTAGTCTGACTGTCTCTGATTTGGAAATCTTACACCTTTTTCCTCGAAAGTTGG  | 1680 |
| Db   | 1633 | TCATGGGTAGTCTGACTGTCTCTGATTTGGAAATCTTACACCTTTTTCCTCGAAAGTTGG  | 1692 |
| Qy   | 1681 | GAATGACCTCTCCAGAAACCTTTAGAGGAGATGCAGAAAGTGAATGGTTCAGATCTGGGA  | 1740 |
| Db   | 1693 | GAATGACCTCTCCAGAAACCTTTAGAGGAGATGCAGAAAGTGAATGGTTCAGATCTGGGA  | 1752 |
| Qy   | 1741 | AAAAAACAGAGACTCAATGAGAGACAGAAAGAAATCCAGGTTCTAATTAAGTGCATTTCT  | 1800 |
| Db   | 1753 | AAAAAACAGAGACTCAATGAGAGACAGAAAGAAATCCAGGTTCTAATTAAGTGCATTTCT  | 1812 |
| Qy   | 1801 | GAAAAAATATTTACCCCATTTGGGAGGTGAAAAACGAAAAAATAACCCCTGGAGAA      | 1860 |
| Db   | 1813 | GAAAAAATATTTACCCCATTTGGGAGGTGAAAAACGAAAAAATAACCCCTGGAGAA      | 1872 |
| Qy   | 1861 | ATTCGTTGTTCCCACTGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT   | 1920 |
| Db   | 1873 | ATTCGTTGTTCCCACTGAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT   | 1932 |
| Qy   | 1921 | ATCAGAAAGTCTGTGTATACAGTAACTGTGATGATTTCTTCCAGATATATGCTTGTCT    | 1980 |
| Db   | 1933 | ATCAGAAAGTCTGTGTATACAGTAACTGTGATGATTTCTTCCAGATATATGCTTGTCT    | 1992 |
| Qy   | 1981 | TTACAAACCAACCATTTTCTAGAGAGTCTCTTACTCATTAATCAATGAATGGATTGGT    | 2040 |
| Db   | 1993 | TTACAAACCAACCATTTTCTAGAGAGTCTCTTACTCATTAATCAATGAATGGATTGGT    | 2052 |
| Qy   | 2041 | AAGATGTCTTGAAGAACATGTTAGTCAGAGACTGTGTAATAATATATTAAGATTAACTC   | 2100 |
| Db   | 2053 | AAGATGTCTTGAAGAACATGTTAGTCAGAGACTGTGTAATAATATATTAAGATTAACTC   | 2112 |
| Qy   | 2101 | ATTTCATATCATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAAT  | 2135 |
| Db   | 2113 | ATTTCATATCATATCAATATCAATATCAATATCAATATCAATATCAATATCAATATCAAT  | 2147 |
| RESULT 13  |      |   |      |
| : Sequence 536, Application us/60258275  |      |   |      |
| : GENERAL INFORMATION:   |      |   |      |
| : APPLICANT: Beasley, Ellen  |      |   |      |
| : TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,                       |      |   |      |
| : TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS |      |   |      |
| : FILE REFERENCE: CLO01026-PROV  |      |   |      |
| : CURRENT APPLICATION NUMBER: us/60/258,275                                      |      |   |      |
| : CURRENT FILING DATE: 2000-12-27  |      |   |      |
| : NUMBER OF SEQ ID NOS: 717  |      |   |      |
| : SOFTWARE: FastSeq for Windows Version 4.0                                      |      |   |      |
| : SEQ ID NO 536  |      |   |      |

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; LENGTH: 2137
; TYPE: DNA
; ORGANISM: HUMAN
US-60-258-275-536

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| Query Match                | 99.3%; | Score 2119.2; | DB 69;    | Length 2137; |
| Best Local Similarity      | 99.8%; | Pred. No. 0;  |           |              |
| Matches 2132; Conservative | 0;     | Mismatches 3; | Indels 1; | Gaps 1;      |

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | CCCCGGCTCGCGCCCCAATTTCTAAAGAGCTGCTGTCGCCCGGAAAGCTTCAACATC      | 60  |
| Db | 2   | CCCCGGCTCGCGCCCCAATTTCTAAAGAGCTGCTGTCGCCCGGAAAGCTTCAACATC      | 61  |
| QY | 61  | CTTGGGAGCGCCCCAGCTACAAAGACACTGTCTTGAAAGCGTGTATCACTCCGTAGTTG    | 120 |
| Db | 62  | CTTGGGAGCGCCCCAGCTACAAAGACACTGTCTTGAAAGCGTGTATCACTCCGTAGTTG    | 121 |
| QY | 121 | CAAGTTTCGAGCGCGCAGTGGGAAGCATGTGGGGACATACAGACGAGGTATGCGCTTCGAG  | 180 |
| Db | 122 | CAAGTTTCGAGCGCGCAGTGGGAAGCATGTGGGGACATACAGAGGTATGCGCTTCGAG     | 181 |
| QY | 181 | GCGAGTGGGGCCCCCTCCAGACGCGCTCATCTTCTCTGTCAGCGGCAGCATATCCCA      | 240 |
| Db | 182 | GCGAGTGGGGCCCCCTCCAGACGCGCTCATCTTCTCTGTCAGCGGCAGCATATCCCA      | 241 |
| QY | 241 | ATGGCTTCATATGATATGTACGTGCTGTCTCTGCGGGGAGACCCCGAGACACGCTGTGAG   | 300 |
| Db | 242 | ATGGCTTCATATGATATGTACGTGCTGTCTCTGCGGGGAGACCCCGAGACACGCTGTGAG   | 301 |
| QY | 301 | TGCCGGACGCGCGCAACTGAGACGCGCTTGCGGCAACAACAGTGTCCCGCTGCGGCTGC    | 360 |
| Db | 302 | TGCCGGACGCGCGCAACTGAGACGCGCTTGCGGCAACAACAGTGTCCCGCTGCGGCTGC    | 361 |
| QY | 361 | GGGACGGCGCGGAGGTGCCCCACAGTGGACGCGCTACCGGCTGCGCAACATCCGCACT     | 420 |
| Db | 362 | GGGACGGCGCGGAGGTGCCCCACAGTGGACGCGCTACCGGCTGCGCAACATCCGCACT     | 421 |
| QY | 421 | TCTCGGCGCTCGGGCTTGAAGCCCGGGCGGACGTGAGACCTGGGGGACGTGGAGCAGAGA   | 480 |
| Db | 422 | TCTCGGCGCTCGGGCTTGAAGCCCGGGCGGACGTGAGACCTGGGGGACGTGGAGCAGAGA   | 481 |
| QY | 481 | GCATCCCGAATGCGCTGGAGATTAGCCAGAGAGCTTACTGTCTACCGTGTGAGCCAGT     | 540 |
| Db | 482 | GCATCCCGAATGCGCTGGAGATTAGCCAGAGAGCTTACTGTCTACCGTGTGAGCCAGT     | 541 |
| QY | 541 | GGAAATCTGATGTGAGAGCAATCTGAAGAGTGCCTCCACACCTCCCTGTTCTTCGAG      | 600 |
| Db | 542 | GGAAATCTGATGTGAGAGCAATCTGAAGAGTGCCTCCACACCTCCCTGTTCTTCGAG      | 601 |
| QY | 601 | GCGTGTCTTCGCGCTCTTCGTGTGTCGGGACAGCTGTACACA-GGTTTGGACAGAGAAC    | 660 |
| Db | 602 | GCGTGTCTTCGCGCTCTTCGTGTGTCGGGACAGCTGTACACAAGGTTTGGGACAGAGAAC   | 661 |
| QY | 660 | GTTTCTCTTCGCAACCAATGGCTGTACAGACTGGCTTCAGATTCTCTCAGATTTTTCACATC | 720 |
| Db | 662 | GTTTCTCTTCGCAACCAATGGCTGTACAGACTGGCTTCAGATTCTCTCAGATTTTTCACATC | 721 |
| QY | 720 | AGCTGGGAGATGTTCACTGTATTGTCATCTGTGGGACATGGGACAGATCTCCAACTAT     | 780 |
| Db | 722 | AGCTGGGAGATGTTCACTGTATTGTCATCTGTGGGACATGGGACAGATCTCCAACTAT     | 781 |
| QY | 780 | GTTGGTAGCCTTCACTATAGGAACAAGAAATCTTGGCAGTCAAGTTCGATATATATTCCT   | 840 |
| Db | 782 | GTTGGTAGCCTTCACTATAGGAACAAGAAATCTTGGCAGTCAAGTTCGATATATATTCCT   | 841 |
| QY | 840 | ACATATAGAGATGACATTTTGTGACAGTTGGCTATATGCTATGCTGCGCACTGTTGCTTAC  | 899 |
| Db | 842 | ACATATAGAGATGACATTTTGTGACAGTTGTGCTATATGCTATGCTGCGCACTGTTGCTTAC | 901 |
| QY | 900 | TTCATACAGAGACTGGGGGATGCTGCTGCTGGCGCTGACAGGTGCGGGAGTGTGTGTGTC   | 959 |
| Db | 902 | TTCATACAGAGACTGGGGGATGCTGCTGCTGGCGCTGACAGGTGCGGGAGTGTGTGTGTC   | 961 |



|    |      |   |      |
|----|------|---|------|
| Db | 541  | CTGTACAGCTGGCTTACAGCTTCCTGCAAGATTTTCTCCATCAGCTGGGAGATGTTCACTG | 600  |
| QY | 739  | TGTTATTTTGTCAATCGTGGGCATAGGGCCAGATCTCCAACTATGTGGTAGCTTCATACAG | 798  |
| Db | 601  | TGTTATTTGTCAATCGTGGGCATAGGGCCAGATCTCCAACTATGTGGTAGCTTCATACAG  | 660  |
| QY | 739  | GAAAGAAATTTTGTGGCAAGTCAGTTCGATTAATATTCCTCAATTAGAGAGTGCACAT    | 858  |
| Db | 661  | GAAAGAAATTTTGTGGCAAGTCAGTTCGATTAATATTCCTCAATTAGAGAGTGCACAT    | 720  |
| QY | 839  | TTTTTGCAGTTGGCTAATATGCTGTGCCACTGTGTTTGCTTACTTCATCAGAGACTGGCGA | 918  |
| Db | 721  | TTTTTGCAGTTGGCTAATATGCTGTGCCACTGTGTTTGCTTACTTCATCAGAGACTGGCGA | 780  |
| QY | 919  | TGCTCTCTGTGGCGGTGAGCGGTGGGGGAGTCTGTGTGTCCCGCTGTGTGTGCTTATTC   | 978  |
| Db | 781  | TGCTCTCTGTGGCGGTGAGCGGTGGGGGAGTCTGTGTGTCCCGCTGTGTGTGCTTATTC   | 840  |
| QY | 979  | CTGAATCTCCCGATGGCTGATATCCACAGAAAGATTAGAGAGCTGCAAGATATATCC     | 1033 |
| Db | 841  | CTGAATCTCCCGATGGCTGATATCCACAGAAAGATTAGAGAGCTGCAAGATATATCC     | 900  |
| QY | 1039 | AAAAAGCTGCAAAAATGAAACAACACAGCTGTACCAAGCTGATATTGTTGTGTGGAG     | 1099 |
| Db | 901  | AAAAAGCTGCAAAAATGAAACAACACAGCTGTACCAAGCTGATATTGTTGTGTGGAG     | 960  |
| QY | 1099 | AGCTAAATCCCTGGAAGCAGCAAGAGCTTTCATCTGTGACCTGTTCAGAGCTGGAAAT    | 1158 |
| Db | 961  | AGCTAAATCCCTGGAAGCAGCAAGAGCTTTCATCTGTGACCTGTTCAGAGCTGGAAAT    | 1022 |
| QY | 1159 | TTGGCATATATACCTTATATGTTCTTGCTGTATGGATCTGACCTGAGTGGGTTACTTGG   | 1218 |
| Db | 1021 | TTGGCATATATACCTTATATGTTCTTGCTGTATGGATCTGACCTGAGTGGGTTACTTGG   | 1080 |
| QY | 1219 | CTGTGTCTGTGGATCTCTTAATTTACATGGAGAGCTTACTGTGAACCTGTTTCCCTGTG   | 1278 |
| Db | 1081 | CTGTGTCTGTGGATCTCTTAATTTACATGGAGAGCTTACTGTGAACCTGTTTCCCTGTG   | 1140 |
| QY | 1279 | CCTTGATTTGAATTTCCAGCTTACATTTACAGCCTGGCTGTATTGGCAAGCTGCCAGGC   | 1338 |
| Db | 1141 | CCTTGATTTGAATTTCCAGCTTACATTTACAGCCTGGCTGTATTGGCAAGCTGCCAGGC   | 1200 |
| QY | 1339 | GTATATATATAGCTGACATGCTGTCTGGGGAGGAGGTGCTTCTTCAATTCATACAGG     | 1398 |
| Db | 1201 | GTATATATATAGCTGACATGCTGTCTGGGGAGGAGGTGCTTCTTCAATTCATACAGG     | 1260 |
| QY | 1399 | TACCTGTGGATTTATCTTCTTATTCCAATGGTCTGTGTCATCTGGGAAAAATTTGGATCA  | 1458 |
| Db | 1261 | TACCTGTGGATTTATCTTCTTATTCCAATGGTCTGTGTCATCTGGGAAAAATTTGGATCA  | 1320 |
| QY | 1459 | CCTGTGCTTTCATGCTGTATATGCTTACATGCTGTGAGCTTACCCAACTCTGGTCAGGA   | 1518 |
| Db | 1321 | CCTGTGCTTTCATGCTGTATATGCTTACATGCTGTGAGCTTACCCAACTCTGGTCAGGA   | 1380 |
| QY | 1519 | ACATGGCGGTGGGGGTACATCCAGGGCTCCAGAAGTGGGAGCATCATCTCCCTACT      | 1578 |
| Db | 1381 | ACATGGCGGTGGGGGTACATCCAGGGCTCCAGAAGTGGGAGCATCATCTCCCTACT      | 1440 |
| QY | 1579 | TTGTATTACTGTGGTCTTACCAAGAAATGCTGCCCTATCATCTCATAGGGTATGCTGACTG | 1638 |
| Db | 1441 | TTGTATTACTGTGGTCTTACCAAGAAATGCTGCCCTATCATCTCATAGGGTATGCTGACTG | 1500 |
| QY | 1639 | TTCGATTTGGAAATCTTACACCTTTTTCCTGGAAAGTTTGGGAATACCTTCCAGAAA     | 1698 |
| Db | 1501 | TTCGATTTGGAAATCTTACACCTTTTTCCTGGAAAGTTTGGGAATACCTTCCAGAAA     | 1560 |
| QY | 1699 | CTTTAGAGCAGATGCAGAAAGTGAATGGTTTCAAGATCTGGGAAAAAACAAGACTCAAA   | 1758 |
| Db | 1561 | CTTTAGAGCAGATGCAGAAAGTGAATGGTTTCAAGATCTGGGAAAAAACAAGACTCAAA   | 1620 |
| QY | 1759 | TGGAGACAGAAAGAAATCCCAAGGTCTTAAATACATGCTATCTGAAAAAATATCTACCCCA | 1818 |
| Db | 1621 | TGGAGACAGAAAGAAATCCCAAGGTCTTAAATACATGCTATCTGAAAAAATATCTACCCCA | 1680 |

| QY | 1819   | TTTTGGTGAAGTCAAAACGAAAAAATTAAGACCCCTGTGAGAAATTCGTTGTTCCCA     | 1874 |
|----|--|---|------|
| Db | 1661   | TTTGCTGAAGTCAAAACGAAAAAATTAAGACCCCTGTGAGAAATTCGTTGTTCCCA      | 1736 |
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|    | US-60-226-176-1990   |   |      |
|    | ; Sequence 1990, Application US/60226176   |   |      |
|    | ; GENERAL INFORMATION:   |   |      |
|    | ; APPLICANT: Ring, Huijun Z.   |   |      |
|    | ; APPLICANT: Malsen, Gareth  |   |      |
|    | ; APPLICANT: Townley, David  |   |      |
|    | ; APPLICANT: Morris, MacDonald   |   |      |
|    | ; TITLE OF INVENTION: Single Nucleotide Polymorphisms Associated With ADME Genes |   |      |
|    | ; FILE REFERENCE: GX-0013-1 P  |   |      |
|    | ; CURRENT APPLICATION NUMBER: US/60/226,176                                      |   |      |
|    | ; NUMBER OF SEQ ID NOS: 2447   |   |      |
|    | ; SOFTWARE: PERL Program   |   |      |
|    | ; SEQ ID NO 1990   |   |      |
|    | ; LENGTH: 1656   |   |      |
|    | ; TYPE: DNA  |   |      |
|    | ; ORGANISM: Homo sapiens   |   |      |
|    | ; FEATURE:   |   |      |
|    | ; NAME/KEY: misc_feature   |   |      |
|    | ; OTHER INFORMATION: GB:AB007448.1   |   |      |
|    | US-60-226-176-1990   |   |      |
|    | Query Match  | 77.6%; Score 1656; DB 66; Length 1656;                        |      |
|    | Best Local Similarity  | 100.0%; Pred. No. 0;  |      |
|    | Matches 1656; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                    |   |      |
| QY | 147  | ATGCGGGACTACGACGAGTGATGCGCTTCCTGSGGAGTGGGGCCCTTCACGCGCTC      | 206  |
| Db | 1  | ATGCGGGGACTACGACGAGTGATGCGCTTCCTGSGGAGTGGGGCCCTTCACGCGCTC     | 60   |
| QY | 207  | ATCTCTTCGCGTCAGGCGGACGATCATCCCAATGGCTTCATGTATGTACGTGTG        | 266  |
| Db | 61   | ATCTCTTCGCGTCAGGCGGACGATCATCCCAATGGCTTCATGTATGTACGTGTG        | 120  |
| QY | 267  | TTCTGTGGGGGAGCCCGGAGACACCGCTGTGATGTCGGAGCAGCGGGAACCTGAGCAGC   | 326  |
| Db | 121  | TTCTGTGGGGGAGCCCGGAGACACCGCTGTGATGTCGGAGCAGCGGGAACCTGAGCAGC   | 180  |
| QY | 327  | GCCGTGGGCAACACAGTGTCCCGCTGCGGCTGCGGGAGCGCCGAGATGCCCCACAGC     | 386  |
| Db | 181  | GCCGTGGGCAACACAGTGTCCCGCTGCGGCTGCGGGAGCGCCGAGATGCCCCACAGC     | 240  |
| QY | 387  | TGCAGCCGCTACCGGCTGCGCACATCGCCAACTTCTCGGGGCTCGGGGCTGAGCCGGGG   | 446  |
| Db | 241  | TGCAGCCGCTACCGGCTGCGCACATCGCCAACTTCTCGGGGCTCGGGGCTGAGCCGGGG   | 300  |
| QY | 447  | CGGACGTTGACCTGGGGGACGTTGGAGCAGAGAGAGCTGCGTGGATGGCTGGGATTCAGC  | 506  |
| Db | 301  | CGGACGTTGACCTGGGGGACGTTGGAGCAGAGAGAGCTGCGTGGATGGCTGGGATTCAGC  | 360  |
| QY | 507  | CAGGACGTCATACCTGTCCACCGTCGTCACCGAGAGGAAATCGTGTGTTGAGACAACTGG  | 566  |
| Db | 361  | CAGGACGTCATACCTGTCCACCGTCGTCACCGAGAGGAAATCGTGTGTTGAGACAACTGG  | 420  |
| QY | 567  | AAGTGGCCCTTCACACCTCCCTGTTGTTGTGATGGGCTGCTCGGCTCCTTCGTGTCC     | 626  |
| Db | 421  | AAGTGGCCCTTCACACCTCCCTGTTGTTGTGATGGGCTGCTCGGCTCCTTCGTGTCC     | 480  |
| QY | 627  | GGGACGCTGTACAGAGGTTTGGCAGAGAAAGCTTCTCTCCAAACCATGCTGTACAG      | 686  |
| Db | 481  | GGGACGCTGTACAGAGGTTTGGCAGAGAAAGCTTCTCTCCAAACCATGCTGTACAG      | 540  |
| QY | 687  | ACTGGGCTTCAGGCTTCGCGAGATTTTTCATCATGAGCGGGAGATGTTCACTGTGTTATTT | 746  |
| Db | 541  | ACTGGGCTTCAGGCTTCGCGAGATTTTTCATCATGAGCGGGAGATGTTCACTGTGTTATTT | 600  |

Search completed: July 5, 2003, 08:28:14  
Job time : 4831 secs

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QY 747 GTCATGTTGGGAGTGGGCGAGATCTCCAACTATGTGGTAGCCCTCATCTAGAACAGAA 806
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Db 601 GTCATGTTGGGAGTGGGCGAGATCTCCAACTATGTGGTAGCCCTCATCTAGAACAGAA 660
QY 807 ATTCTTGGCAAGTCATTTGTTATATATCTCTACTTAGAGTGTGCACATTTTWTGCA 866
    |||||||
Db 661 ATTCTTGGCAAGTCATTTGTTATATATCTCTACTTAGAGTGTGCACATTTTWTGCA 720
QY 867 GTTGGCTATATGCTGTGCGACTGTGTGCTTACTTCTATCATGAGAGTGGCGGATGCTGCG 926
    |||||||
Db 721 GTTGGCTATATGCTGTGCGACTGTGTGCTTACTTCTATCATGAGAGTGGCGGATGCTGCG 780
QY 927 CTGGCGCTACGCGTGGGAGTGTGTGTCCGCTGTGGTGTGTTCAATTCCTGAATCT 986
    |||||||
Db 781 CTGGCGCTACGCGTGGGAGTGTGTGTCCGCTGTGGTGTGTTCAATTCCTGAATCT 840
QY 987 CCCCCGATGGCTGATATCCAGAGAAATTTAGAGAGGCTGAAGATATCATCCAAAAGCT 1046
    |||||||
Db 841 CCCCCGATGGCTGATATCCAGAGAAATTTAGAGAGGCTGAAGATATCATCCAAAAGCT 900
QY 1047 GCAAAATGAAACACACAGCTGTACCGAGTATATTGATTCGTGGAGGAGCTAAAT 1106
    |||||||
Db 901 GCAAAATGAAACACACAGCTGTACCGAGTATATTGATTCGTGGAGGAGCTAAAT 960
QY 1107 CCCCAGAACAGCAGAAAGCTTTCATTCGTGACCTGTTCAGGACTCGAAATATGCGATA 1166
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Db 961 CCCCAGAACAGCAGAAAGCTTTCATTCGTGACCTGTTCAGGACTCGAAATATGCGATA 1020
QY 1167 ATGACCATATATGCTTGTGCTATGATGCTGACCTCAGTGGGTTACTTGTCTGTCT 1226
    |||||||
Db 1021 ATGACCATATATGCTTGTGCTATGATGCTGACCTCAGTGGGTTACTTGTCTGTCT 1080
QY 1227 CTGATGTCTCTAATTTACATGAGATGCTTACCTGACTGTTTCTCTGCTGCTGAT 1286
    |||||||
Db 1081 CTGATGTCTCTAATTTACATGAGATGCTTACCTGACTGTTTCTCTGCTGCTGAT 1140
QY 1287 GAAATTCAGCTTACATTTACAGCTGTGCTATTGCGAACCTGCCAGGCGTTATATC 1346
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Db 1141 GAAATTCAGCTTACATTTACAGCTGTGCTATTGCGAACCTGCCAGGCGTTATATC 1200
QY 1347 ATAGCTGAGTACTGTCTGCGGAGAGGAGTGTCTGCTTCTGATTCAACTGTAACCTGTG 1406
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Db 1201 ATAGCTGAGTACTGTCTGCGGAGAGGAGTGTCTGCTTCTGATTCAACTGTAACCTGTG 1260
QY 1407 GATTAATTAATTCATTCATTTGCTGTGCTATGCTGAGAAAATTGGATCACTGTGCT 1466
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Db 1261 GATTAATTAATTCATTCATTTGCTGTGCTATGCTGAGAAAATTGGATCACTGTGCT 1320
QY 1467 TTCTCCATGCTATATGCTTCACTGCTGAGCTCTAACCAACCTGTGCGAACAATGGCG 1526
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Db 1321 TTCTCCATGCTATATGCTTCACTGCTGAGCTCTAACCAACCTGTGCGAACAATGGCG 1380
QY 1527 GTGGGGGTACATCCACGCGCTCCAGAGTGGGAGAGCATCATTTGCCCTTACTTGTAC 1586
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Db 1381 GTGGGGGTACATCCACGCGCTCCAGAGTGGGAGAGCATCATTTGCCCTTACTTGTAC 1440
QY 1587 CTGCGTGTACACAGAAATGCTGCCCTACATGCTATGAGGTAGTCTGACTGTCTGAT 1646
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Db 1441 CTGCGTGTACACAGAAATGCTGCCCTACATGCTATGAGGTAGTCTGACTGTCTGAT 1500
QY 1647 GGAATCTTACCCCTTTTTCCTTGAAGTTGGGAATGACTTTCAGAAAACCTTAGAG 1706
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Db 1501 GGAATCTTACCCCTTTTTCCTTGAAGTTGGGAATGACTTTCAGAAAACCTTAGAG 1560
QY 1707 CAGATGCAAGAAAGTGAATGTTGATCTGGGAAAAAACAAGAGACTCAATGAGACA 1766
    |||||||
Db 1561 CAGATGCAAGAAAGTGAATGTTGATCTGGGAAAAAACAAGAGACTCAATGAGACA 1620
QY 1767 GAAGAAATCCCAAGTTCTAATAACTCATTTCTGA 1802
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Db 1621 GAAGAAATCCCAAGTTCTAATAACTCATTTCTGA 1656
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 07:02:38 ; Search time 1582 Seconds  
(without alignments)  
9657.709 Million cell updates/sec

Title: US-09-521-195b-2

Perfect score: 2135  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8255821 seqs, 3578102051 residues

Total number of hits satisfying chosen parameters: 16511642

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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19: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq3:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID                  | Description        |
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| 1          | 2130.2 | 99.8        | 2135   | US-10-170-235-41510 | Sequence 41510, A  |
| 2          | 2130.2 | 99.8        | 2135   | US-10-327-189-1     | Sequence 1, Appl1  |
| 3          | 2103.4 | 98.5        | 2136   | US-10-327-189-1     | Sequence 37, Appl1 |
| 4          | 1940.4 | 90.9        | 2343   | US-09-724-676-48345 | Sequence 48345, A  |
| 5          | 1940.4 | 90.9        | 2343   | US-09-724-676-48345 | Sequence 48345, A  |
| 6          | 1310.6 | 61.4        | 2080   | US-10-144-771-9909  | Sequence 9909, Ap  |
| 7          | 1065.8 | 48.9        | 3252   | US-09-949-016-438   | Sequence 438, App  |
| 8          | 1064.2 | 47.9        | 3252   | US-10-327-189-3     | Sequence 438, App  |
| 9          | 1023   | 47.9        | 3223   | US-09-949-016-2058  | Sequence 2058, Ap  |
| 10         | 1016.2 | 47.6        | 3223   | US-10-170-235-41508 | Sequence 41508, A  |
| 11         | 1016.2 | 47.6        | 3223   | US-60-453-135-4827  | Sequence 4827, Ap  |
| 12         | 1016.2 | 47.6        | 3223   | US-60-453-050-4827  | Sequence 4827, Ap  |
| 13         | 1016.2 | 47.6        | 3223   | US-60-456-412-4827  | Sequence 4827, Ap  |

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|----|-------|------|-------|----|---------------------|--------------------|
| 14 | 994   | 46.6 | 2574  | 14 | US-10-144-771-9977  | Sequence 9977, Ap  |
| 15 | 982.8 | 46.0 | 3037  | 2  | PCT-US03-03482-3472 | Sequence 3472, Ap  |
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| 17 | 982.8 | 46.0 | 3037  | 14 | US-10-301-856-969   | Sequence 969, App  |
| 18 | 982.8 | 46.0 | 3037  | 15 | US-10-357-507-3472  | Sequence 3472, Ap  |
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| 20 | 905.6 | 42.4 | 2297  | 14 | US-10-144-771-9906  | Sequence 9906, Ap  |
| 21 | 905.6 | 42.4 | 2297  | 15 | US-10-326-820-1     | Sequence 1, Appl1  |
| 22 | 539   | 25.2 | 692   | 15 | US-10-170-235-34118 | Sequence 34118, A  |
| 23 | 539   | 25.2 | 692   | 15 | US-60-466-412-85914 | Sequence 85914, A  |
| 24 | 526.4 | 24.7 | 54550 | 15 | US-10-327-189-42    | Sequence 42, Appl1 |
| 25 | 393   | 18.4 | 393   | 15 | US-09-170-235-27867 | Sequence 27867, A  |
| 26 | 364.8 | 17.1 | 29871 | 11 | US-10-949-016-12180 | Sequence 12180, A  |
| 27 | 364.8 | 17.1 | 29876 | 11 | US-09-949-016-13800 | Sequence 13800, A  |
| 28 | 364   | 17.0 | 37876 | 19 | US-60-466-412-85911 | Sequence 85911, A  |
| 29 | 360.2 | 16.9 | 614   | 15 | US-10-327-189-8     | Sequence 8, Appl1  |
| 30 | 360.2 | 16.9 | 26850 | 15 | US-10-327-189-41    | Sequence 41, Appl1 |
| 31 | 247.6 | 11.6 | 475   | 2  | PCT-US03-13853-2908 | Sequence 2908, Ap  |
| 32 | 195.6 | 9.2  | 2152  | 14 | US-10-152-319A-1921 | Sequence 1921, Ap  |
| 33 | 195.6 | 9.2  | 2152  | 14 | US-10-301-856-1080  | Sequence 1080, Ap  |
| 34 | 194.8 | 9.1  | 2480  | 18 | US-60-453-135-6288  | Sequence 6288, Ap  |
| 35 | 194.8 | 9.1  | 2480  | 18 | US-60-453-050-6288  | Sequence 6288, Ap  |
| 36 | 194.8 | 9.1  | 2480  | 19 | US-60-466-412-6288  | Sequence 6288, Ap  |
| 37 | 193.6 | 9.1  | 1725  | 2  | PCT-US02-19592-27   | Sequence 27, Appl1 |
| 38 | 193.6 | 9.1  | 2257  | 2  | PCT-US02-29560-58   | Sequence 58, Appl1 |
| 39 | 193.6 | 9.1  | 2257  | 2  | PCT-US02-19592-26   | Sequence 26, Appl1 |
| 40 | 193.6 | 9.1  | 2257  | 14 | US-10-245-882-58    | Sequence 58, Appl1 |
| 41 | 193.6 | 9.1  | 2257  | 16 | US-10-295-027-299   | Sequence 299, App  |
| 42 | 193.6 | 9.1  | 2480  | 15 | US-10-170-235-22149 | Sequence 22149, A  |
| 43 | 193   | 9.0  | 2138  | 14 | US-10-144-771-7194  | Sequence 7194, Ap  |
| 44 | 188.2 | 8.8  | 2403  | 10 | US-09-724-676-47336 | Sequence 47336, A  |
| 45 | 188.2 | 8.8  | 2403  | 10 | US-09-724-676-47336 | Sequence 47336, A  |

## ALIGNMENTS

RESULT 1  
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; Sequence 41510, Application US/10170235  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU  
; FILE REFERENCE: C1001380  
; CURRENT APPLICATION NUMBER: US/10/170, 235  
; CURRENT FILING DATE: 2003-03-17  
; NUMBER OF SEQ ID NOS: 42514  
; SEQ ID NO 41510  
; LENGTH: 2135  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-170-235-41510

Query Match 99.8%; Score 2130.2; DB 15; Length 2135;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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| QY | 1   | CCCCGGCTTCGCGCCCAATTTCTACAGCCTGCTGCTCCCGGGAGAGCTTACATC 60  |
| DB | 1   | CCCCGGCTTCGCGCCCAATTTCTACAGCCTGCTGCTCCCGGGAGAGCTTACATC 60  |
| QY | 61  | CTTGGGAGGAGCCCGACCTACAGACCTCTCGAGAGCGTGCATACCGGTGTTG 120   |
| DB | 61  | CTTGGGAGGAGCCCGACCTACAGACCTCTCTGAGAGCGTGCATACCGGTGTTG 120  |
| QY | 121 | CAAGTTTCGAGGCGGAGTGGAGAGCATGCGGAGCTACGAGAGTGCCTTCTGG 180   |
| DB | 121 | CAAGTTTCGAGGCGGAGTGGAGAGCATGCGGAGCTACGAGAGTGCCTTCTGG 180   |
| QY | 181 | CGAGTGGGAGGCGCTTCCAGCGCTATCTTCTCTGCTGACGCGCAGCATATCCCA 240 |
| DB | 181 | CGAGTGGGAGGCGCTTCCAGCGCTATCTTCTCTGCTGACGCGCAGCATATCCCA 240 |

|    |      |  |      |
|----|------|--|------|
| QY | 241  | ATGCTTCGAAGATGATGCACTGCTGTTTCCGTGGGGGGAGACCCCGGAGACCGCTGTGAG   | 300  |
| Db | 241  | ATGGCTTCGAAGATGATGCACTGCTGTTTCCGTGGGGGGAGACCCCGGAGACCGCTGTGAG  | 300  |
| QY | 301  | TGCGCGAGCGCGCAACCTGTAGCAGCGCGCTGGCGCAACACATGATGCCGTGGGGCTGC    | 360  |
| Db | 301  | TGCCGGAAGCGCGCAACCTGTAGCAGCGCGCTGGCGCAACACATGATGCCGTGGGGCTGC   | 360  |
| QY | 361  | GGGACGGCGCGGAGAGTGCCTCCACAGCTGACAGCCGTACCCGCTGGCCACATGGCAACT   | 420  |
| Db | 361  | GGGACGGCGCGGAGAGTGCCTCCACAGCTGACAGCCGTACCCGCTGGCCACATGGCAACT   | 420  |
| QY | 421  | TCTGGCGCTGGGCTGGAGCCGGGGCGCGACGTGAGACTGGGGCAGCTGGAGCAGAGA      | 480  |
| Db | 421  | TCTGGCGCTGGGCTGGAGCCGGGGCGCGACGTGAGACTGGGGCAGCTGGAGCAGAGA      | 480  |
| QY | 481  | GCTCCCTGAGATGCTGGAGTTTCAGCCAGAGCTTCACCTGTCCACCGCTGTGACCGAGT    | 540  |
| Db | 481  | GCTCCCTGAGATGCTGGAGTTTCAGCCAGAGCTTCACCTGTCCACCGCTGTGACCGAGT    | 540  |
| QY | 541  | GGAAATCGAGTGTGAGAGCAACAGGAAAGGGCCCTCACCACTCCCTGTTCCTGAG        | 600  |
| Db | 541  | GGAAATCGAGTGTGAGAGCAACAGGAAAGGGCCCTCACCACTCCCTGTTCCTGAG        | 600  |
| QY | 601  | GCGTGTCTCTGGGCTCTTCTGCTGCCGGGCGAGCTGTGAGACAGGTTTTGGCAGGAAGACG  | 660  |
| Db | 601  | GCGTGTCTCTGGGCTCTTCTGCTGCCGGGCGAGCTGTGAGACAGGTTTTGGCAGGAAGACG  | 660  |
| QY | 661  | TTTCTCTTGCACACATGGCTGTACAGACTGGCTTCAGCTCTCTGCAGATTTTCTTCATCA   | 720  |
| Db | 661  | TTTCTCTTGCACACATGGCTGTACAGACTGGCTTCAGCTCTCTGCAGATTTTCTTCATCA   | 720  |
| QY | 721  | GCTGGGAGATTTCACTGTGTTATTTGTGCATCGGGGATGGGCGACATGCCAATCTG       | 780  |
| Db | 721  | GCTGGGAGATTTCACTGTGTTATTTGTGCATCGGGGATGGGCGACATGCCAATCTG       | 780  |
| QY | 781  | TGATGACCTTCATCTAGAGAACAGAAATTTCTTGGCAAGTCAGTTGTATTAATTTCTCTA   | 840  |
| Db | 781  | TGATGACCTTCATCTAGAGAACAGAAATTTCTTGGCAAGTCAGTTGTATTAATTTCTCTA   | 840  |
| QY | 841  | CATTAGGAGTGTGCACATTTTTCAGTGTGGCTTATGCTGCTGCACATGTTGCTTACT      | 900  |
| Db | 841  | CATTAGGAGTGTGCACATTTTTCAGTGTGGCTTATGCTGCTGCACATGTTGCTTACT      | 900  |
| QY | 901  | TCATCAGAGACTGGCGGATGCTGCTGTGCGCTGACGAGTCCCGGAGTGGCTGTGTCC      | 960  |
| Db | 901  | TCATCAGAGACTGGCGGATGCTGCTGTGCGCGCTGACGAGTCCCGGAGTGGCTGTGTCC    | 960  |
| QY | 961  | CGCTGTGGTGTCTATTCCTGAATCTCCCGATGGCTATATCCACAGGAAGATTTAGS       | 1020 |
| Db | 961  | CGCTGTGGTGTCTATTCCTGAATCTCCCGATGGCTATATCCACAGGAAGATTTAGS       | 1020 |
| QY | 1021 | AGGCTGAAGATATCATCCAAAAGCTGCAGAAAATGACACACAGACTGTACACAGATGA     | 1080 |
| Db | 1021 | AGGCTGAAGATATCATCCAAAAGCTGCAGAAAATGACACACAGACTGTACACAGATGA     | 1080 |
| QY | 1081 | TATTTGATTTCTGTGAGAGAGCTAAATCCCTGGAAGCAGACAGAACTTTCATTTGACAC    | 1140 |
| Db | 1081 | TATTTGATTTCTGTGAGAGAGCTAAATCCCTGGAAGCAGACAGAACTTTCATTTGACAC    | 1140 |
| QY | 1141 | TGTTCCAGAGACTCGGAATATTTGCCATATGACCAATTATGTCTTTGTGCTATGATGCTGA  | 1200 |
| Db | 1141 | TGTTCCAGAGACTCGGAATATTTGCCATATGACCAATTATGTCTTTGTGCTATGATGCTGA  | 1200 |
| QY | 1201 | CCCTAGTGGGTACTTTGCTCTGCTCTGATGAGTGTCCCTAATTTACATGAGAGATGCCATCC | 1260 |
| Db | 1201 | CCCTAGTGGGTACTTTGCTCTGCTCTGATGAGTGTCCCTAATTTACATGAGAGATGCCATCC | 1260 |
| QY | 1261 | TGAACGTGTTCTCTCTGCTGCTTGAATTCAGATTAACATTAACAGCTGGCTGCTAT       | 1320 |
| Db | 1261 | TGAACGTGTTCTCTCTGCTGCTTGAATTCAGATTAACATTAACAGCTGGCTGCTAT       | 1320 |

|  |      |   |      |
|--|------|---|------|
| QY   | 1321 | GGGCAAGCGTCCCGAGCGTTATATCAATAGCTGAGTACAGTCTGCTGGGAGGAGGTGCG       | 1380 |
| Db   | 1321 | TGGCAACCCCTGGCCAGCGTTATATCAATAGCTGAGTACAGTCTGCTGGGAGGAGGTGCG      | 1380 |
| QY   | 1381 | TTCTCTTCATTCACAACTGGTACCTGCTGGATTAATTAATCTTAATCCATTGGTCTGGTCAATGC | 1440 |
| Db   | 1381 | TTCTCTTCATTCACAACTGGTACCTGCTGGATTAATTAATCTTAATCCATTGGTCTGGTCAATGC | 1440 |
| QY   | 1441 | TGGGAAAAATTTGGGATCAACCTCTGCTTTCTTCACATGCGTATGCTTCTTACATGCTGAGCTCT | 1500 |
| Db   | 1441 | TGGGAAAAATTTGGGATCAACCTCTGCTTTCTTCACATGCGTATGCTTCTTACATGCTGAGCTCT | 1500 |
| QY   | 1501 | ACCCAAACCCCTGCTGAGAACATGCGGCTGGGAGGTACATCCAGCGCCCTCCAGATGCGGCA    | 1560 |
| Db   | 1501 | ACCCAAACCCCTGCTGAGAACATGCGGCTGGGAGGTACATCCAGCGCCCTCCAGATGCGGCA    | 1560 |
| QY   | 1561 | GCATCATTTGCCCTTACTTTGTTTAACTCGGTGCTTAACACAGATGCTGCTCAATCG         | 1620 |
| Db   | 1561 | GCATCATTTGCCCTTACTTTGTTTAACTCGGTGCTTAACACAGATGCTGCTCAATCG         | 1620 |
| QY   | 1621 | TCATGGGTAGTCTACATGCTCCTGATTTGGAAATCTTACACCCCTTTTTCCTCGAAAGTTGG    | 1680 |
| Db   | 1621 | TCATGGGTAGTCTACATGCTCCTGATTTGGAAATCTTACACCCCTTTTTCCTCGAAAGTTGG    | 1680 |
| QY   | 1681 | GAATGACTCTTCCAGAAAACCTTAGAGACAGATGCGAAAAGTCAAAATGGTTGATGATCTGGGA  | 1740 |
| Db   | 1681 | GAATGACTCTTCCAGAAAACCTTAGAGACAGATGCGAAAAGTCAAAATGGTTGATGATCTGGGA  | 1740 |
| QY   | 1741 | AAAAAACAGAGACTCAATGAGAGACAGAAAGAAATCCCAAGTCTTAATACTGCATTTCT       | 1800 |
| Db   | 1741 | AAAAAACAGAGACTCAATGAGAGACAGAAAGAAATCCCAAGTCTTAATACTGCATTTCT       | 1800 |
| QY   | 1801 | GAAGAAATATTTACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCCCTGTGGAGAA     | 1860 |
| Db   | 1801 | GAAGAAATATTTACCCCATTTGGTGAAGTGAAGAAACAGAAATTAAGACCCCTGTGGAGAA     | 1860 |
| QY   | 1861 | ATTCGTTGTTCCCACTGTAATGAGACTGACTGTAAACGATGACACCAAAATGAACTTGCT      | 1920 |
| Db   | 1861 | ATTCGTTGTTCCCACTGTAATGAGACTGACTGTAAACGATGACACCAAAATGAACTTGCT      | 1920 |
| QY   | 1921 | ATCAAGAAATCTGCTCATACAGTAAGTAACTGGATGATTTCTTCAGATTAATGTCCTTGCT     | 1980 |
| Db   | 1921 | ATCAAGAAATCTGCTCATACAGTAAGTAACTGGATGATTTCTTCAGATTAATGTCCTTGCT     | 1980 |
| QY   | 1981 | TTACAAACCAACCAATTTCTAGAGAGTCTCTTACTATTAATTAATGAATGATTTGGT         | 2040 |
| Db   | 1981 | TTACAAACCAACCAATTTCTAGAGAGTCTCTTACTATTAATTAATGAATGATTTGGT         | 2040 |
| QY   | 2041 | AAGATGCTTGAAGAAACATGTTAGTCAAGAGATGGTAAATATCAATTAAGATTAACTGC       | 2100 |
| Db   | 2041 | AAGATGCTTGAAGAAACATGTTAGTCAAGAGATGGTAAATATCAATTAAGATTAACTGC       | 2100 |
| QY   | 2101 | ATTTCAATCATACAAATACTATCCAAATAAAAAAT                               | 2135 |
| Db   | 2101 | ATTTCAATCATACAAATACTATCCAAATAAAAAAT                               | 2135 |
| RESULT 2   |      |   |      |
| US-10-327-189-1  |      |   |      |
| : Sequence 1, Application US/10327189  |      |   |      |
| : GENERAL INFORMATION:   |      |   |      |
| : APPLICANT: Pelekovaya, Vanya D   |      |   |      |
| : APPLICANT: Whittle, Richard F  |      |   |      |
| : APPLICANT: Rubin, Laurence A   |      |   |      |
| : APPLICANT: Peter, St George-Hyslop H   |      |   |      |
| : APPLICANT: Simionovitch, Katherine A   |      |   |      |
| : TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOC |      |   |      |
| : FILE REFERENCE: EILP-020   |      |   |      |
| : CURRENT APPLICATION NUMBER: US/10/327,189  |      |   |      |
| : CURRENT FILING DATE: 2002-12-20  |      |   |      |
| : PRIOR APPLICATION NUMBER: 60/362,700   |      |   |      |
| : PRIOR FILING DATE: 2002-03-08  |      |   |      |

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; PRIOR APPLICATION NUMBER: 60/343,338
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/427,529
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/362,717
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2214
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (166)..(1821)
; OTHER INFORMATION:
US-10-327-189-1

Query Match      99.8%; Score 2130.2; DB 15; Length 2214;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      20  CCCCAGCTTCGCGCCGCCCAATTTCTACAGCCTGCTGCCCGGGAACTTCTACATC 79
QY      61  CTGGGGAGCGCCCGAGCTACAGACACTGTCAGAGAGCGTGTACACCGTAGTGTG 120
DB      80  CTGGGGAGCGCCCGAGCTACAGACACTGTCAGAGAGCGTGTACACCGTAGTGTG 139
QY      121  CAAGTTTCGAGAGCGGCACTGGGAAACATGCGGGACTACAGAGAGTGTGCTCTCTG 180
DB      140  CAAGTTTCGAGAGCGGCACTGGGAAACATGCGGGACTACAGAGAGTGTGCTCTCTG 199
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QY      361  GGGAGGCGCGGAGGTGCGCCACAGCTGACGCGCTACCGGCTGGCCACTTGGCCAACT 420
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QY      481  GCTGCGCTGATGGCTGGAGGTTCAAGCCAGAGAGTCTACCTGTCCACCGTCTGTACCG 540
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DB      560  GGAATCTGTGTGTAGAGACAACCTGGAAGGTGCCCTTACCACTCCCTGTTCTTCTAG 619
QY      601  GCGTCTCTCTCGGCTCTTCTGTGTCGGGAGCTGTACAGAGGTTGGGAGGAAGAG 660
DB      620  GCGTCTCTCTCGGCTCTTCTGTGTCGGGAGCTGTACAGAGGTTGGGAGGAAGAG 679
QY      661  TTCTCTTTCGCAACATGAGCTGTACAGACTGAGCTTCTCTCTCTCTCTCTCTCTCT 720
DB      680  TTCTCTTTCGCAACATGAGCTGTACAGACTGAGCTTCTCTCTCTCTCTCTCTCTCT 739
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DB      740  GCTGGAGATGTTCACCTGTGTATTTGTATCTGTGTGAGATGGGCCATGTCTCAACTAT 799
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QY      781  TGGAGCCTTCATACCTAGAGAAATTTCTGGCAAGTCAGTTCGATTAATTTCTCTA 840
DB      800  TGGAGCCTTCATACCTAGAGAAATTTCTGGCAAGTCAGTTCGATTAATTTCTCTA 859
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DB      860  CATTAGAGTGTGCACATTTTTCAGTTGGCTATATGCTGTCCACCTGTTTGTCTACT 919
QY      901  TCATCAGAGACTGGCGGATCTGCTGTGGCGCTGACGGTGCCTGGAGAGTGTGTGTCC 960
DB      920  TCATCAGAGACTGGCGGATCTGCTGTGGCGCTGACGGTGCCTGGAGAGTGTGTGTCC 979
QY      961  CGCTGTGGTTCATTCCTGAATTCGCCGATGCGATATCCAGAGAAATTTAGAG 1020
DB      980  CGCTGTGGTTCATTCCTGAATTCGCCGATGCGATATCCAGAGAAATTTAGAG 1039
QY      1021  AGGCTGAAGATATCATCCAAAAGCTGCAAAATGAAACAACAGCTGTACAGCAGTGA 1080
DB      1040  AGGCTGAAGATATCATCCAAAAGCTGCAAAATGAAACAACAGCTGTACAGCAGTGA 1099
QY      1081  TATTTGATTTGTGGAGAGCTAAATCCCTGAAGACAGAAAGCTTTCATTTGTGACC 1140
DB      1100  TATTTGATTTGTGGAGAGCTAAATCCCTGAAGACAGAAAGCTTTCATTTGTGACC 1159
QY      1141  TGTTCAGAGCTCGGAATATTTGCCATATATGACATTAATGCTTGTGTATGAGATCTGA 1200
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DB      1280  TGAACGTTCCTCTCTGCGCTGTATGAAATTCACACTTACATTAAGCTGCTGCTAT 1339
QY      1321  TGGCAAGCTGCGCAGCGCTTATATCATACCTCAGTACTGTTCTGGGGAGAGGTGTGC 1380
DB      1340  TGGCAAGCTGCGCAGCGCTTATATCATACCTCAGTACTGTTCTGGGGAGAGGTGTGC 1399
QY      1381  TTCTCTTCATTCACATGTGATCTGTGATTTACTTCTTATTCATTTGCTGTGATCG 1440
DB      1400  TTCTCTTCATTCACATGTGATCTGTGATTTACTTCTTATTCATTTGCTGTGATCG 1459
QY      1441  TGGGAAAATTTGGGATACCTGTCTTCTTCTCAATGCTGTATGTCTTCACTGCTGAGCTCT 1500
DB      1460  TGGGAAAATTTGGGATACCTGTCTTCTTCTCAATGCTGTATGTCTTCACTGCTGAGCTCT 1519
QY      1501  ACCCAACCTGTGTCAGGAACATGCGGCTGGGGGTCAATCCAGGCGCTCCAGAGTGGGA 1560
DB      1520  ACCCAACCTGTGTCAGGAACATGCGGCTGGGGGTCAATCCAGGCGCTCCAGAGTGGGA 1579
QY      1561  GCATCATTTGCCCTTACTTTTGTATCTCTGCTTCAACAAGATGTGCCCTACATCG 1620
DB      1580  GCATCATTTGCCCTTACTTTTGTATCTCTGCTTCAACAAGATGTGCCCTACATCG 1639
QY      1621  TCATGGGTATGTGATGCTGCTGATTTGGAATCTTCAACCTTTTTCCTGAAAAGTTTG 1680
DB      1640  TCATGGGTATGTGATGCTGCTGATTTGGAATCTTCAACCTTTTTCCTGAAAAGTTTG 1699
QY      1681  GAATGACTTTCAGAAAACCTTAGAGCAGATGAGAAAAGTAATGTTTCAGATCTGGGA 1740
DB      1700  GAATGACTTTCAGAAAACCTTAGAGCAGATGAGAAAAGTAATGTTTCAGATCTGGGA 1759
QY      1741  AAAAAACAGAGACTCAATGAGAGACAGAAAATCCCAAGGTTCTAATTAATGCTACTCT 1800
DB      1760  AAAAAACAGAGACTCAATGAGAGACAGAAAATCCCAAGGTTCTAATTAATGCTACTCT 1819
QY      1801  GAAAAAATATCTACCCCATTTGTTGTAAGTAAAAACAGAAAATTAAGACCTCTGGAGAA 1860
DB      1820  GAAAAAATATCTACCCCATTTGTTGTAAGTAAAAACAGAAAATTAAGACCTCTGGAGAA 1879
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FEATURE:
NAME/KEY: misc_feature
LOCATION: (327)..(327)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (328)..(328)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (330)..(330)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (331)..(331)
OTHER INFORMATION: n can be a or t or g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (334)..(334)

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[illegible]

QY 301 TGCCGAGCGCCGACCTGAGACGCGCTGGCGCAACAGTGTCCCGCTGGCGCTGC 360  
 DB 301 TGCCGAGCGCCGACCTGAGACGCGCTGGCGCAACAGTGTCCCGCTGGCGCTGC 360  
 QY 361 GGGAGCGCGCGAGGTGCGCCACAGCTGACGCGCTGACCGCTGCGCAACT 420  
 DB 361 GGGAGCGCGCGAGGTGCGCCACAGCTGACGCGCTGACCGCTGCGCAACT 420  
 QY 421 TCTGCGCGCTGGCGCTGAGCGCGCGCGAGCGTGGCGCGTGGCGAGTGGAGAGA 480  
 DB 421 TCTGCGCGCTGGCGCTGAGCGCGCGCGAGCGTGGCGCGTGGCGAGTGGAGAGA 480  
 QY 481 GCTGCGCTGAGTGGCTGGAGTTCAGCCAGGAGCTGACCTGCGCCGCTGAGAGT 540  
 DB 481 GCTGCGCTGAGTGGCTGGAGTTCAGCCAGGAGCTGACCTGCGCCGCTGAGAGT 540  
 QY 541 GGAATCTGTGTGTGAGAGCAACTGGAAAGTGGCCCTCCACACCTCTGTTTTCGTAG 600  
 DB 541 GGAATCTGTGTGTGAGAGCAACTGGAAAGTGGCCCTCCACACCTCTGTTTTCGTAG 600  
 QY 601 GCGTCTGCTGCGGCTCTTCTGCTGCGCGGAGCTGTGACAGAGTGGCGAGGAAGC 660  
 DB 601 GCGTCTGCTGCGGCTCTTCTGCTGCGCGGAGCTGTGACAGAGTGGCGAGGAAGC 660  
 QY 661 TTCTCTTGCAACCATGAGCTGTGACAGCTGCGCTTCACTCTGAGATTTTCTCCATCA 720  
 DB 661 TTCTCTTGCAACCATGAGCTGTGACAGCTGCGCTTCACTCTGAGATTTTCTCCATCA 720  
 QY 721 GCTGGGAGATGTTCACCTGTGTATTTGTATCTGCTGAGGAGTGGCGCAATCTCCAACTAG 780  
 DB 721 GCTGGGAGATGTTCACCTGTGTATTTGTATCTGCTGAGGAGTGGCGCAATCTCCAACTAG 780  
 QY 781 TGTGTGCGCTTCTACTAGAGCAAGAAATTTCTGCGAGCGAGTGTATTTATCTCTA 840  
 DB 781 TGTGTGCGCTTCTACTAGAGCAAGAAATTTCTGCGAGCGAGTGTATTTATCTCTA 840  
 QY 841 CATTAAGAGTGTGACAAATTTTTCAGAGTGGCTATATGCTGCTGACAGTGTGCTTACT 900  
 DB 841 CATTAAGAGTGTGACAAATTTTTCAGAGTGGCTATATGCTGCTGACAGTGTGCTTACT 900  
 QY 901 TCAATGAGAGTGGCGGAGTGTGCTGCTGCGCTGACGCTGCGGAGTGTGCTGCTG 960  
 DB 901 TCAATGAGAGTGGCGGAGTGTGCTGCTGCGCTGACGCTGCGGAGTGTGCTGCTG 960  
 QY 961 CGCTGAGTGTGCTTCTGCTGATCTCCCGATGGCTGATCTCCAGAGAAATTTAGAG 1020  
 DB 961 CGCTGAGTGTGCTTCTGCTGATCTCCCGATGGCTGATCTCCAGAGAAATTTAGAG 1020  
 QY 1021 AGGCTGAGATATCATCCAAAAAGCTGCAAAAATGACAAACAGCTGTACAGAGTGA 1080  
 DB 1021 AGGCTGAGATATCATCCAAAAAGCTGCAAAAATGACAAACAGCTGTACAGAGTGA 1080  
 QY 1081 TATTTGATCTGTGAGAGGAGTAAATCCCTGAGAGAGAGAAACCTTCAATTCGAGAC 1140  
 DB 1081 TATTTGATCTGTGAGAGGAGTAAATCCCTGAGAGAGAGAAACCTTCAATTCGAGAC 1140  
 QY 1141 TGTTCAGAGTGTGAGATATTTGCCAATATGACATTAATGCTTGTGCTATGAGTCTGA 1200  
 DB 1141 TGTTCAGAGTGTGAGATATTTGCCAATATGACATTAATGCTTGTGCTATGAGTCTGA 1200  
 QY 1201 CCTGAGTGGTACTTGTCTGTCTGTGATGCTGCTTCAATTTACATGAGAGTGCCTAC 1260  
 DB 1201 CCTGAGTGGTACTTGTCTGTCTGTGATGCTGCTTCAATTTACATGAGAGTGCCTAC 1260  
 QY 1261 TGAAGCTTCTGCTGCTGCTGATGAGATTCAGAGTGTGCTGAGTGTGCTGCTGCTAT 1320  
 DB 1261 TGAAGCTTCTGCTGCTGCTGATGAGATTCAGAGTGTGCTGAGTGTGCTGCTGCTAT 1320  
 QY 1321 TGGGAAGCTGTGCCAGGCTTATATCATAGCTGACAGTGTGCTGCTGCTGCTGCTGCT 1380  
 DB 1321 TGGGAAGCTGTGCCAGGCTTATATCATAGCTGACAGTGTGCTGCTGCTGCTGCTGCT 1380

QY 1381 TTCTCTTCAATCACTGTGACCTGTGAGTATTAATCTTCTTATCATTTGCTGTGATCC 1440  
 DB 1381 TTCTCTTCAATCACTGTGACCTGTGAGTATTAATCTTCTTATCATTTGCTGTGATCC 1440  
 QY 1441 TGGGAATTTTGGGATTCACCTGCTTCTTCCATGCTGATGCTTCACTGCTGAGCTCT 1500  
 DB 1441 TGGGAATTTTGGGATTCACCTGCTTCTTCCATGCTGATGCTTCACTGCTGAGCTCT 1500  
 QY 1501 ACCCAACCTGTGTGAGAGTATGAGTGGGAGTCAATCAACAGGCTCCAGAGTGGGA 1560  
 DB 1501 ACCCAACCTGTGTGAGAGTATGAGTGGGAGTCAATCAACAGGCTCCAGAGTGGGA 1560  
 QY 1561 GCATCATTTGCGCCCTACTTGTATTACCTGCTGCTTACAAGATGCTGCTACATG 1620  
 DB 1561 GCATCATTTGCGCCCTACTTGTATTACCTGCTGCTTACAAGATGCTGCTACATG 1620  
 QY 1621 TCAATGCTGCTGAGTGTGCTGCTGATGAGTCTTCAACCTTTTTCCTGAAAGTTGG 1680  
 DB 1621 TCAATGCTGCTGAGTGTGCTGCTGATGAGTCTTCAACCTTTTTCCTGAAAGTTGG 1680  
 QY 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGCAAGAAAGTGAATGCTGAGTGGGA 1740  
 DB 1681 GAATGACTTTCAGAAACCTTAGAGCAGATGCAAGAAAGTGAATGCTGAGTGGGA 1740  
 QY 1741 AAAAACAAGAGTCTCAATGAGACAGAAAGAAATCCCAAGTCTTCAATTAATGCTGCT 1800  
 DB 1741 AAAAACAAGAGTCTCAATGAGACAGAAAGAAATCCCAAGTCTTCAATTAATGCTGCT 1800  
 QY 1801 GAAAAAATATCTACCCCATTTTGTGAGTGAAGTGAAGAAATTAAGACCTGTGAGAA 1860  
 DB 1801 GAAAAAATATCTACCCCATTTTGTGAGTGAAGTGAAGAAATTAAGACCTGTGAGAA 1860  
 QY 1861 ATTGCTGTTCCTCACTGAGTGAATGAGTGTGATGAGTGAAGTGAAGTGAAGTGAAGT 1920  
 DB 1861 ATTGCTGTTCCTCACTGAGTGAATGAGTGTGATGAGTGAAGTGAAGTGAAGTGAAGT 1920  
 QY 1921 ATCAAGAAATGCTGCTGATACAGTAAACTGAGTGTGCTTCCAGATATGCTGCTGCT 1980  
 DB 1921 ATCAAGAAATGCTGCTGATACAGTAAACTGAGTGTGCTTCCAGATATGCTGCTGCT 1980  
 QY 1981 TTCAAAACCAACATTTCTAGAGAGTCTCCTTACTCAATTAATCAATGAATGAGTGT 2040  
 DB 1981 TTCAAAACCAACATTTCTAGAGAGTCTCCTTACTCAATTAATCAATGAATGAGTGT 2040  
 QY 2041 AAGATGCTTGAAGAAATGTTAGTCAAGAGTGTGTAATTAATTAATTAATTAATTAAT 2100  
 DB 2041 AAGATGCTTGAAGAAATGTTAGTCAAGAGTGTGTAATTAATTAATTAATTAATTAAT 2100  
 QY 2101 ATTT-CCATATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2136  
 DB 2101 ATTTCCAAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2136

## RESULT 4

US-09-724-676-48345  
 ; Sequence 48345, Application US/09724676  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Compugen LTD  
 ; TITLE OF INVENTION: Variants of alternative splicing  
 ; FILE REFERENCE: 129181.4 Compugen  
 ; CURRENT APPLICATION NUMBER: US/09/724,676  
 ; CURRENT FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 97222  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 48345  
 ; LENGTH: 2343  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-724-676-48345

Query Match 90.9%; Score 1940.4; DB 10; Length 2343;  
 Best Local Similarity 92.1%; Pred. No. 0;  
 Matches 2134; Conservative 1; Indels 183; Gaps 1;

QY 1 CCCGCGCTGCGCGCCCAATTTCTAACAGCGCTGCTGTCCCGCGGAGAGTTCTAACATC 60  
Db 1 CCCCGGCTTGCGCGCCCAATTTCTAACAGCGCTGCTGTCCCGCGGAGAGTTCTAACATC 60  
QY 61 CTTGGGAGCGCCCGACCTTACAAAGACACTGTCTGTGAAGCGTGTATCAACCCGTAGTTG 120  
Db 61 CTTGGGAGCGCCCGACCTTACAAAGACACTGTCTGTGAAGCGTGTATCAACCCGTAGTTG 120  
QY 121 CAAGTTTCGAGGCGGCGAGTGGGAAGCATGGGGACATACGACGAGTGTATCGCTTCTCGG 180  
Db 121 CAAGTTTCGAGGCGGCGAGTGGGAAGCATGGGGACATACGACGAGTGTATCGCTTCTCGG 180  
QY 181 GCGAGTGGGGGCCCTTCCAGCGGCTCATTTCTTCCGTGACAGCGCAGATATCCCA 240  
Db 181 GCGAGTGGGGGCCCTTCCAGCGGCTCATTTCTTCCGTGACAGCGCAGATATCCCA 240  
QY 241 ATGGCTTCATATGATATGTAGTGTGTCTGTGCGGGGAGCCCGGAGCACCGCTGTGAG 300  
Db 241 ATGGCTTCATATGATATGTAGTGTGTCTGTGCGGGGAGCCCGGAGCACCGCTGTGAG 300  
QY 301 TGCGGAGCGCGCGCAACTGAGCAGCGCTGGCGCAACAAGTGTCCGCTGCGGCTGC 360  
Db 301 TGCGGAGCGCGCGCAACTGAGCAGCGCTGGCGCAACAAGTGTCCGCTGCGGCTGC 360  
QY 361 GGGAGCGCGCGAGGTGCCACAGCTGCAGCCGCTACCGGCTGCGCACCATTGCGCACT 420  
Db 361 GGGAGCGCGCGAGGTGCCACAGCTGCAGCCGCTACCGGCTGCGCACCATTGCGCACT 420  
QY 421 TCTCGGCGCTGCGGGGCGGAGCGCGGGGCGGAGCTGAGACCTGGGGGCGCTGGAGCAGAGA 480  
Db 421 TCTCGGCGCTGCGGGGCGGAGCGCGGGGCGGAGCTGAGACCTGGGGGCGCTGGAGCAGAGA 480  
QY 481 GCTGCGCTGATGAGTGGGAGTTCAGCCAGGAGCTGACCTGTCCACCGCTGAGCGAGT 540  
Db 481 GCTGCGCTGATGAGTGGGAGTTCAGCCAGGAGCTGACCTGTCCACCGCTGAGCGAGT 540  
QY 541 GGAATCTGGTGTGAGGACAACTGGAAGTGTGCCCCACACCTTCCCTGTCTGTAG 600  
Db 541 GGAATCTGGTGTGAGGACAACTGGAAGTGTGCCCCACACCTTCCCTGTCTGTAG 600  
QY 601 GCGTGTCTCGGCTCCTTCTGTGTCCGGGAGCTGTACAGAGTGTGGCAGGAAGAAAG 660  
Db 601 GCGTGTCTCGGCTCCTTCTGTGTCCGGGAGCTGTACAGAGTGTGGCAGGAAGAAAG 660  
QY 661 TTCTCTTCCCAACCATGGCTGTACAGACTGGCTCAGCTTCCGAGATTTCTCCATCA 720  
Db 661 TTCTCTTCCCAACCATGGCTGTACAGACTGGCTCAGCTTCCGAGATTTCTCCATCA 720  
QY 721 GCTGGAGAGTTCACCTGTATTTGTCATGTGGGCAATGGGCCAGATCTCCAACTATG 780  
Db 721 GCTGGAGAGTTCACCTGTATTTGTCATGTGGGCAATGGGCCAGATCTCCAACTATG 780  
QY 781 TGGTAGCCTTCACTACTAGGACAGAAATTTCTGGCAAGTCACTGTATATATCTCTA 840  
Db 781 TGGTAGCCTTCACTACTAGGACAGAAATTTCTGGCAAGTCACTGTATATATCTCTA 840  
QY 841 CATTAGAGATGTGCACATTTTTCAGATTTGCTATATGTCTGTGCTGCTACT 900  
Db 841 CATTAGAGATGTGCACATTTTTCAGATTTGCTATATGTCTGTGCTGCTACT 900  
QY 901 TCATCAGAGACTGGGGATGTGTGTGCGTGTGCGTGTGCGTGTGCTGTGCTG 960  
Db 901 TCATCAGAGACTGGGGATGTGTGTGCGTGTGCGTGTGCGTGTGCTGTGCTG 960  
QY 961 CGCTGTGGT----- 969  
Db 961 CGCTGTGGT----- 969  
QY 970 ----- 969  
Db 970 ----- 969  
QY 1021 GACTTGGCCCAAGAGAGCCAGCTGGGAGCCAGCACTGACAAAGCTGAGTGTCCCTG 1080

QY 970 ----- 969  
Db 1081 AACATTTCACAGTGTCTTACCATTTTCTTATATAAAGAAATAGCTTCTTGTGAAATC 1140  
QY 970 ----- 969  
Db 1141 CCATCTGGGAGGTTCATTTCTGTGAATCTCCCGCATGGCTGATATCCAGAGAAATTTA 1200  
QY 1018 GAGAGCGTGAAGATATTCATCCAAAAGCTGCAAAAATATACACACAGCTGTACAGCAG 1077  
Db 1201 GAGAGCGTGAAGATATTCATCCAAAAGCTGCAAAAATATACACACAGCTGTACAGCAG 1260  
QY 1078 TGATATTTGATTTCTGTGAGAGAGCTAAATCCCTTAACAGAGAAAGCTTCAATTCGG 1137  
Db 1261 TGATATTTGATTTCTGTGAGAGAGCTAAATCCCTTAACAGAGAAAGCTTCAATTCGG 1320  
QY 1138 ACCTGTTCAGACTGCGAATATTTGCCATTAATGACCATTAATGCTTGTGCTGATGATGC 1197  
Db 1321 ACCTGTTCAGACTGCGAATATTTGCCATTAATGACCATTAATGCTTGTGCTGATGATGC 1380  
QY 1198 TGACCTCAGTGGGTACTTGTCTGTCTGTGATGCTCTAATTTATACATGAGATGCT 1257  
Db 1381 TGACCTCAGTGGGTACTTGTCTGTCTGTGATGCTCTAATTTATACATGAGATGCT 1440  
QY 1258 ACCTGAATGTTTCTCTCTGCTGATTTGAATTCAGCTTACATTAACAGCTGCGTGC 1317  
Db 1441 ACCTGAATGTTTCTCTCTGCTGATTTGAATTCAGCTTACATTAACAGCTGCGTGC 1500  
QY 1318 TATTGCGAAGCTGCGCCAGCGGTTATATCATAGCTGCAGTACTGTTCTGGGAGAGAGTG 1377  
Db 1501 TATTGCGAAGCTGCGCCAGCGGTTATATCATAGCTGCAGTACTGTTCTGGGAGAGAGTG 1560  
QY 1378 TGCTTCTTCAATTCATGTTGATGCTGATTTATTTCTTATTCATTTGCTGTGCTCA 1437  
Db 1561 TGCTTCTTCAATTCATGTTGATGCTGATTTATTTCTTATTCATTTGCTGTGCTCA 1620  
QY 1438 TGCTGGGAAATTTGGGATCAGCTGTCTGCTTCTCAGCTGTATGTCTTCACTGTGAGC 1497  
Db 1621 TGCTGGGAAATTTGGGATCAGCTGTCTGCTTCTCAGCTGTATGTCTTCACTGTGAGC 1680  
QY 1498 TCTAACCAACCTGTGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1557  
Db 1681 TCTAACCAACCTGTGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1740  
QY 1558 GCAGCATATTTGCCCTTACTTTGTTTACTCTGCTGTCTTACACAGAACTGCTGCCATCA 1617  
Db 1741 GCAGCATATTTGCCCTTACTTTGTTTACTCTGCTGTCTTACACAGAACTGCTGCCATCA 1800  
QY 1618 TCGTCATGGGTAGTCTGACTGTCTGATTTGGAATCTTACCCCTTTTTCCTGAAAGTT 1677  
Db 1801 TCGTCATGGGTAGTCTGACTGTCTGATTTGGAATCTTACCCCTTTTTCCTGAAAGTT 1860  
QY 1678 TGGGAATGACTCTTCCAGAAACCTTAGAGAGATGCGAAGTGGAAATGGTTCAGATCTG 1737  
Db 1861 TGGGAATGACTCTTCCAGAAACCTTAGAGAGATGCGAAGTGGAAATGGTTCAGATCTG 1920  
QY 1738 GGAAGAAACAGAGACTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797  
Db 1921 GGAAGAAACAGAGACTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
QY 1798 TCTGAAAAAATATATACCCATTTTGGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 1957  
Db 1981 TCTGAAAAAATATATACCCATTTTGGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2040  
QY 1858 GAAATTTGTTTCCCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1917  
Db 2041 GAAATTTGTTTCCCTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2100  
QY 1918 GCTATCAAGAAATGCTGTATACAGTAAATCTGTGATGATTTCTTCCAGATATATGCTCT 1977  
Db 2101 GCTATCAAGAAATGCTGTATACAGTAAATCTGTGATGATTTCTTCCAGATATATGCTCT 2160  
QY 1978 GCTTTACAAACCAACATTTTCTAGAGAGTCTCTTACTCATTTATTTCAATGAAATGAT 2037

| Accession | Sequence  | Position |
|-----------|---|----------|
| Dc        | 2161 GCTTTACAAACCAACCTTTCTAGAGAGTCTCCTACTCATTAATTCAATCAAAATGGATT    | 2220     |
| Qy        | 2038 GGTAAAGATGTCCTTGAAACATGTTAGTCAAGAGACTGGTAAAAATACATATAAAGATTACA | 20977    |
| Dc        | 2221 GGTAAGATGTCCTTGAAACATGTTAGTCAAGAGACTGGTAAAAATACATATAAAGATTACA  | 2280     |
| Qy        | 2098 CTCATTTCCAATCATCAAAATACATCAAAATATAAAAT                         | 2135     |
| Dc        | 2281 CTCATTTCCAATCATCAAAATACATCAAAATATAAAAT                         | 2318     |

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RESULT 5
US-09-724-676A-48345
; Sequence 48345, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48345
; LENGTH: 2343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-48345

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| Query Match           | 90.9%          | Score 1940.4  | DB 10      | Length 2343 |
|-----------------------|----------------|---|------------|-------------|
| Best Local Similarity | 92.1%          | Pred. No. 0   |            |             |
| Matches 2134          | Conservative 0 | Mismatches 1  | Indels 183 | Gaps 1      |
| QY                    | 1              | CCCCGGCTTCGCGCCCCCAATTTCTAACAGCCTGCCTGTCCCCCGGGAAAGTTCTAACATC | 60         |             |
| DB                    | 1              | CCCCGGCTTCGCGCCCCCAATTTCTAACAGCCTGCCTGTCCCCCGGGAAAGTTCTAACATC | 60         |             |
| QY                    | 61             | CTTGGGGAGCCCCCAGCTACAAGACACTGTCTCTGAGAACGCTGTATCACCCTGATTTG   | 120        |             |
| DB                    | 61             | CTTGGGGAGCCCCCAGCTACAAGACACTGTCTCTGAGAACGCTGTATCACCCTGATTTG   | 120        |             |
| QY                    | 121            | CAAGTTTGGAGAGCGCAGTGGGAAAGCATGCGGAGACTAGACAGAGGTGATGCGCTCTGG  | 180        |             |
| DB                    | 121            | CAAGTTTGGAGAGCGCAGTGGGAAAGCATGCGGAGACTAGACAGAGGTGATGCGCTCTGG  | 180        |             |
| QY                    | 181            | GCGAGTGGGGGCCCTTCCAGCGCCTCATCTTTCTTCTGTCTCAGCGCCACGATCATCCCA  | 240        |             |
| DB                    | 181            | GCGAGTGGGGGCCCTTCCAGCGCCTCATCTTTCTTCTGTCTCAGCGCCACGATCATCCCA  | 240        |             |
| QY                    | 241            | ATGGCTTCAATGTATGTACGTACGTCTGCTTCTGGCGGGACCCCGGAGACCGCTGTCCAG  | 300        |             |
| DB                    | 241            | ATGGCTTCAATGTATGTACGTACGTCTGCTTCTGGCGGGACCCCGGAGACCGCTGTCCAG  | 300        |             |
| QY                    | 301            | TGCCGAGAGCGCGCAACTGAGACAGCGCTGGCGGAACAACAGTGTCCCGCTGCGCGTGC   | 360        |             |
| DB                    | 301            | TGCCGAGAGCGCGCAACTGAGACAGCGCTGGCGGAACAACAGTGTCCCGCTGCGCGTGC   | 360        |             |
| QY                    | 361            | GGGAGAGCGCGGAGGTGCCCCACAGCTGCAGCGCTACCGGCTGCACACATCCGCAACT    | 420        |             |
| DB                    | 361            | GGGAGAGCGCGGAGGTGCCCCACAGCTGCAGCGCTACCGGCTGCACACATCCGCAACT    | 420        |             |
| QY                    | 421            | TCTGGGCGCTGGGCGCTGAGAGCGGGGCGGAGCTGGAGCTGGGGAGAGTGGAGACAGGGA  | 480        |             |
| DB                    | 421            | TCTGGGCGCTGGGCGCTGAGAGCGGGGCGGAGCTGGAGCTGGGGAGAGTGGAGACAGGGA  | 480        |             |
| QY                    | 481            | GCTGCGCTGATGAGTGGGAGTTCAACACAGAGACTTACTGTCCACCGTCCGACCGAGT    | 540        |             |
| DB                    | 481            | GCTGCGCTGATGAGTGGGAGTTCAACACAGAGAGTCTACTGTCCACCGTCCGACCGAGT   | 540        |             |
| QY                    | 541            | GGAATCTGGTGTGTAGAGCAACTGGAAGTCCCTTACCACTTCCTCTTCTGTGAG        | 600        |             |
| DB                    | 541            | GGAATCTGGTGTGTAGAGCAACTGGAAGTCCCTTACCACTTCCTCTTCTGTGAG        | 600        |             |

|    |      |       |  |       |  |     |
|----|------|-------|--|-------|--|-----|
| QY | 601  | GC    | GTG  | CTCT  | CGGCTCTTCTGCTGTCCGGGACAGCTGTACAGACAGTTTGGCAGGAAGACG  | 660 |
| Db | 601  | GC    | GTG  | CTCT  | CGGCTCTTCTGCTGTCCGGGACAGCTGTACAGACAGTTTGGCAGGAAGAACG | 660 |
| QY | 661  | TT    | CTCTTGGCAACCATGGCTGTACAGATGGCTTCAGCTTCCTCAGATTTCCTCAGATTTCACATCA | 720   |  |     |
| Db | 661  | TT    | CTCTTGGCAACCATGGCTGTACAGATGGCTTCAGCTTCCTCAGATTTCCTCAGATTTCACATCA | 720   |  |     |
| QY | 721  | GC    | TGGAGATGTACACTGTATTATTTGTTCATCGTGGGATGGGACAGATCTCCAACTATG        | 780   |  |     |
| Db | 721  | GC    | TGGAGATGTACACTGTATTATTTGTTCATCGTGGGATGGGACAGATCTCCAACTATG        | 780   |  |     |
| QY | 781  | TGT   | TAACCTCATACTAGGAACAGAAATCTTGGCAAGTCACTTCGTATTATTTCTCTA           | 840   |  |     |
| Db | 781  | TGT   | TAACCTCATACTAGGAACAGAAATCTTGGCAAGTCACTTCGTATTATTTCTCTA           | 840   |  |     |
| QY | 841  | CATT  | AGAGTGTGCACATTTTTCAGTGTGGCTATATGCTGTGCGACATGTTCCTACT             | 900   |  |     |
| Db | 841  | CATT  | AGAGTGTGTGCACATTTTTCAGTGTGGCTATATGCTGTGCGACATGTTCCTACT           | 900   |  |     |
| QY | 901  | TC    | ATCAGAGATGGGCGATGTGTCGTCGGGCGCTGACAGGATCCCGGAGATGCTGTGTGCC       | 960   |  |     |
| Db | 901  | TC    | ATCAGAGATGTCGGGAGATGTGTCGTCGGGCGCTGACAGGATCCCGGAGATGCTGTGTGCC    | 960   |  |     |
| QY | 961  | CG    | GTGTGT   | ----- | 969  |     |
| Db | 961  | CG    | GTGTGTGTGAGTGTTCATGATGCTCTGCTGTGGCATACTGTACCAAGACAG              | 1020  |  |     |
| QY | 970  | ----- | -----  | ----- | 969  |     |
| Db | 1021 | GAC   | TTGCCCCACAGACAGAGGCCAGCCTGGGACCCAGCATGTACAGAGCTGAGTCTCCCTG       | 1080  |  |     |
| QY | 970  | ----- | -----  | ----- | 969  |     |
| Db | 1081 | AAC   | ATTACAGTGTCTTACCATTTTCTCTATAAAGAAATATAGCTTCTCTGACATC             | 1140  |  |     |
| QY | 970  | ----- | -----  | ----- | 1017   |     |
| Db | 1141 | CC    | ATCCTTGGCAGGTTCATCTTCGATCTCCCGATGGCTGATATCCAGAGAAAGATTTA         | 1200  |  |     |
| QY | 1018 | GAG   | AGGCTGGAAGTATTCATCCAAAAAGTGCMAAAATGAACAACACACCTGTACACAGCAG       | 1077  |  |     |
| Db | 1201 | GAG   | AGGCTGGAAGATTCATCCAAAAAGTGCMAAAATGAACAACACACCTGTACACAGCAG        | 1266  |  |     |
| QY | 1078 | TG    | ATATTGATCTGTGAGAGAGCTAAATCCCTGAACAGACAGAAACCTTTCATCTCGG          | 1137  |  |     |
| Db | 1261 | TG    | ATATTGATCTGTGAGAGAGCTAAATCCCTGAACAGACAGAAACCTTTCATCTCGG          | 1322  |  |     |
| QY | 1138 | ACC   | TTTCAGAGCTGGAAATATGGCATATGACCATATATGTCTTGTCTGATGATGC             | 1197  |  |     |
| Db | 1321 | ACC   | TTTCAGAGCTGGAAATATGGCATATATGACCATATATGTCTTGTCTGATGATGC           | 1380  |  |     |
| QY | 1198 | TA    | ACCTCAGTGGTACTTGTCTGTCTGTGAGATGCTCCATATTTACATGGAATGGCT           | 1257  |  |     |
| Db | 1381 | TA    | ACCTCAGTGGTACTTGTCTGTCTGTGAGATGCTCCATATTTACATGGAATGGCT           | 1440  |  |     |
| QY | 1258 | ACC   | TGAACCTGTTCCCTGTGCTTGTGATTTGAATTCACAGCTTACATTAACAGCTGGTGC        | 1317  |  |     |
| Db | 1441 | ACC   | TGAACCTGTTCCCTGTGCTTGTGATTTGAATTCACAGCTTACATTAACAGCTGGTGC        | 1500  |  |     |
| QY | 1318 | TAT   | TGGAGACGCTGCCAGCGCTATATCATATGCTCAGTACTGTCTGGGGAGAGGNG            | 1377  |  |     |
| Db | 1501 | TAT   | TGGAGACGCTGCCAGCGCTATATCATATGCTCAGTACTGTCTGGGGAGAGGNG            | 1566  |  |     |
| QY | 1378 | TG    | CTCTCTTCATTTCAACTGGTACTGTGATATTTACTTCTTATTCATTTGGTCTGTGCA        | 1433  |  |     |
| Db | 1561 | TG    | CTCTCTCTTCATTTCAACTGGTACTGTGATATTTACTTCTTATTCATTTGGTCTGTGCA      | 1620  |  |     |
| QY | 1438 | TG    | CTGGGAAATTTTGGGATCACCTGTGCTTTCATGCTGTATGTATGCTTCACTGTGTGAC       | 1497  |  |     |
| Db | 1621 | TG    | CTGGGAAATTTTGGGATCACCTGTGCTTTCATGCTGTATGTATGCTTCACTGTGTGAC       | 1688  |  |     |
| QY | 1498 | TC    | TACCAACCTGTGTAGGAACATGGCGGTGGGGGTACATCCAGGCTTCCAGATGG            | 1557  |  |     |

Db 1681 TCTACCCACCCCTGGTGGAGACATGGCGGTGGGGGACATCCAGCGCCCTCCAGAGTGG 1740  
QY 1558 GCAGCATCATTTGCCCTACTTTGTTTACCTCGGTGCTTACAAACAGATGCTCCCTTACA 1617  
Db 1741 GCAGCATCATTTGCCCTACTTTGTTTACCTCGGTGCTTACAAACAGATGCTCCCTTACA 1800  
QY 1618 TCCGATGAGGTGAGTCTACGTCTGCTGATTTGGAATCTTACACCCCTTTTTCCTGAAAGTT 1677  
Db 1801 TCGTCATGGGTGAGTCTACGTCTGCTGATTTGGAATCTTACACCCCTTTTTCCTGAAAGTT 1860  
QY 1678 TGGGAATGACTCTTCCAGAAACCTTACAGAGATGAGAGAGTGAAGTGGTGTAGATGAG 1737  
Db 1861 TGGGAATGACTCTTCCAGAAACCTTACAGAGATGAGAGAGTGAAGTGGTGTAGATGAG 1920  
QY 1738 GGAAGAAACAGAGACTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797  
Db 1921 GGAAGAAACAGAGACTCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980  
QY 1798 TCTGAAAAAATATCTACCCCTATTGGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAG 1857  
Db 1981 TCTGAAAAAATATCTACCCCTATTGGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2040  
QY 1858 GAAATTCGTGTTCCCTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1917  
Db 2041 GAAATTCGTGTTCCCTCCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2100  
QY 1918 GCTATCAAGAAATGCTGCTCATACAGTAAACCTGATGATTTCTTCAGATATGCTCT 1977  
Db 2101 GCTATCAAGAAATGCTGCTCATACAGTAAACCTGATGATTTCTTCAGATATGCTCT 2160  
QY 1978 GCTTTCACAAACCAACATTTCTGAGAGTCTCTTACTATTAATTAATTAATTAATTAAT 2037  
Db 2161 GCTTTCACAAACCAACATTTCTGAGAGTCTCTTACTATTAATTAATTAATTAATTAAT 2220  
QY 2038 GGTAGATGCTCTGAAACATGTTAGTCAAGAGTCTGTAAGTCAATATTAAGATTAACA 2097  
Db 2221 GGTAGATGCTCTGAAACATGTTAGTCAAGAGTCTGTAAGTCAATATTAAGATTAACA 2280  
QY 2098 CTCATTTCCATATATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2135  
Db 2281 CTCATTTCCATATATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2318

RESULT 6  
US-10-144-771-9909  
; Sequence 9909, Application US/10144771  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig  
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF  
; FILE REFERENCE: CL001321  
; CURRENT APPLICATION NUMBER: US/10/144,771  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 47235  
; SEQ ID NO 9909  
; LENGTH: 2080  
; TYPE: DNA  
; ORGANISM: HUMAN  
; US-10-144-771-9909

Query Match 61.4%; Score 1310.6; DB 14; Length 2080;  
Best Local Similarity 85.7%; Pred. No. 4,4e-303;  
Matches 1470; Conservative 0; Mismatches 239; Indels 6; Gaps 1;

QY 137 AATGGAGACATGCGGAGCTACAGAGGTGATCGCTTCCTGCGGCGAGTGGGCGCCTT 196  
Db 109 AGGTGGAACATGCGGAGCTACAGAGGTGATCGCTTCCTGCGGCGAGTGGGCGCCTT 168  
QY 197 CCAGGCGCTCATCTTCTCTCTGCTGAGCGCCAGCATATCCCAATGCGCTTCAATGTAT 256  
Db 169 CCAGGCGCTCATCTTCTCTCTGCTGAGCGCCAGCATATCCCAATGCGCTTCAATGTAT 228  
QY 257 GTCAGTGTGTTCTGCGGCGGAGACCCGAGACACGCGTGTGAGAGTCCGAGACCGCGCAA 316

Db 229 GTCAGTGTGTTCTGCGGCGGAGACCCGAGACACCGTTGCGCTGTTCTGTACACTGTGAA 288  
QY 317 CCGAGACAGCGCTGGCGGACACAGATGCTCCGCTGGGCTGCGGAGACGCGGAGAGT 376  
Db 289 CCGAGACAGCGCTGGCGGACACAGATGCTCCGCTGGGCTGCGGAGACGCGGAGAGT 348  
QY 377 GCCCCACAGCTGACCGCGTACCGGCTGCGGACATCCCAATCTTCTGCGGCGTGGGCT 436  
Db 349 GCCCTAGAGCTGCCCGCGGTACGACCTGGCCACATGCGCAACTCTCTGGAGTGGGCT 408  
QY 437 GGAGCGGCGGCGGACAGTGGAGCTTGGGCGAGCTGAGAGAGAGAGAGAGAGAGAGAG 496  
Db 409 GGAGCGGCGGCGGACAGTGGAGCTTGGGCGAGCTGAGAGAGAGAGAGAGAGAGAGAG 468  
QY 497 GGAGTTCAGCCGACGCTTACCTGTCCACCGCTGTGACCGAGTGGAGATCGAGTGTGA 556  
Db 469 GGAGTTCAGCCGACGCTTCTCTGTCACCATCTGTGACAGAGTGGAGATCTGTGTGA 528  
QY 557 GGACAACTGGAAGTGGCCCTCCACACCTCCCTGTTCTTCTGAGCGGTCTCGGCTC 616  
Db 529 GGATGACTGGAAGACACCCCTCCACACCTCCCTGTTCTTCTGAGCGGTCTCTCGGCTC 588  
QY 617 CTTCGTGTCGCGGCGAGCTGTGAGACAGTGGGCGAGAGAGAGAGAGAGAGAGAGAG 676  
Db 589 CTTCGTGTCGCGGCGAGCTGTGAGACAGTGGGCGAGAGAGAGAGAGAGAGAGAGAG 648  
QY 677 GGCCTACAGAGCTGAGCTTCAAGCTTCCAGATTTCTTCACATGAGTGGAGAGTGTAC 736  
Db 649 GGCCTACAGAGCTGAGCTTCAAGCTTCTGTCAATATTTCTTCACACCACTGGGAGATGTAC 708  
QY 737 TGTGTTATTTGTCATGCTGGGCGATGGGCGAGATCTCCAACTATGTGTGAGCTTCATACT 796  
Db 709 TGTGTTATTTGTCATGCTGGGCGATGGGCGAGATCTCCAACTATGTGTGAGCTTCATACT 768  
QY 797 AGGAACAAATTTCTGGCAAGTCAATGCTGATATATCTCTACATTTAGAGAGTGTAC 856  
Db 769 AGGAACAAATTTCTGGCAAGTCAATGCTGATATATCTCTACATTTAGAGAGTGTAC 828  
QY 857 ATTTTTCAGTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916  
Db 829 ATTTTTCAGTGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 888  
QY 917 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976  
Db 889 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948  
QY 977 TCCGAAATCTCCCGAGTGGCTGATATCCCAAGAGATTTAGAGAGCTGAAGATATCAT 1036  
Db 949 TCCGAAATCTCCCGAGTGGCTGATATCCCAAGAGATTTAGAGAGCTGAAGATATCAT 1008  
QY 1037 CCAAAAAGCTGCAAAAATGAGACACAGCTGTACCGAGAGTATTTGATTTCTGTGG- 1095  
Db 1009 CCAAAAAGCTGCAAAAATGAGACACAGCTGTACCGAGAGTATTTGATTTCTGTGAG- 1068  
QY 1096 -----AGAGCTAAATCCCTGGAAGCAGCAGAGAAAGCTTCAATTTGAGACCTGTTACAGAC 1150  
Db 1069 GCTACAGAGAGCTAAATCCCTGGAAGCAGCAGAGAAAGCTATTAATCTGAGACCTGTTACAGAC 1128  
QY 1151 TCGGAATATTTGCTGATGAGCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1210  
Db 1129 TCGGAATATTTGCTGATGAGCATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188  
QY 1211 TTACTTTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270  
Db 1189 TTACTTTGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248  
QY 1271 CCTCTGCTGCTGATGGAATTTCCAGCTTACATTAACAGCTGCTGCTATTTGGAAGCT 1330  
Db 1249 CCTCTGCTGCTGATGGAATTTCCAGCTTACATTAACAGCTGCTGCTATTTGGAAGCT 1308  
QY 1331 GCCAGGCGTTATATCATAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1390





[illegible]

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Query Match:          47.9%; Score 1023; DB 11; Length 3223;
Best Local Similarity 76.6%; Pred. No. 3.8e-234;
Matches 1289; Conservative 0; Mismatches 370; Indels 24; Gaps 2;

100 CGCTGCATCACCCCTAGTTCGAGTTTCGAGCGCGAGTGGGAGACATCCGGGACTACG 159
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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|    |      |  |      |
|----|------|--|------|
| Db | 175  | CGGGTTCCCGAACCACAGGCGCGCTGTGGGCCCTCTAGGGCGGCACATGCGGACTACG     | 234  |
| QY | 160  | ACGAGGTGATCCGCTTCTGTGGGAGTGGGGGCCCTTCACAGCGCTCATCTTCTCTGC      | 219  |
| Db | 235  | ACGAGGTGACCGCCTTCTGTGGGAGATGGGGGCCCTTCAGGCGCTCATCTTCTCTGC      | 294  |
| QY | 220  | TCAGGCGCCAGTCATCCCCCAATGGGTTCAATGGTATGTCAGTCGCTTCGGGGGGGA      | 279  |
| Db | 295  | TCAGGCGCCAGTCATCCCCCAATGGGTTCAACGGGCTGTCTCCGCTTCTCTGATAGCA     | 354  |
| QY | 280  | CCCCGAGCACCGCTGTGAGTGCGGAGCGCCGCAACTGAGACAGCGCTGGCGACAA        | 339  |
| Db | 355  | CCCCGAGCACCGCTGTGAGTGCGGAGCGCCGCAACTGAGACAGCGCTGGCGACAA        | 414  |
| QY | 340  | ACAGTGTCCCGGTGGGGGCTGGGGGAGCGCGGAGGTTGGCCCCACAGCTACACCGCTACG   | 399  |
| Db | 415  | ACAGTGTCCCGGTGGGGGCTGGGGGAGCGCGGAGGTTGGCCCCACAGCTACACCGCTACG   | 474  |
| QY | 400  | GGCTGCGCCACATTCGCCAATCTCTGCGGCTCGGGGTGGAGGCCGGGGCCGAGCTGAGAC   | 459  |
| Db | 475  | GGCTGCGCCACATTCGCCAATCTCTGCGGCTCGGGGTGGAGGCCGGGGCCGAGCTGAGAC   | 534  |
| QY | 460  | TGGGGCAGTGGAGCAGAGAGACTGCTGCTGGATGCTGGGAGTTCAAGCAGAGCTTACG     | 519  |
| Db | 535  | TGGGGCAGTGGAGCAGAGAGACTGCTGCTGGATGCTGGGAGTTCAATCAGAGCTTACG     | 594  |
| QY | 520  | TGTCCACCGTCTGACCCGAGTGGAAATCTGGTGTGTAGGACACATGGAGAGTGGCCCTCA   | 579  |
| Db | 595  | TGTCCACCGTCTGACCCGAGTGGAAATCTGGTGTGTAGGACACATGGAGAGTGGCCCTCA   | 636  |
| QY | 580  | CCACCTCCCTGTTTCTGTAAGCGTGTCTCGGCTCCTTGTGTCCGGGAGCTGTGAG        | 639  |
| Db | 637  | CATCTCCCTGTTTCTGTAAGCGTGTCTCGGCTCCTTGTGTCCGGGAGCTGTGAG         | 696  |
| QY | 640  | ACAGTGTGGCAGGAAGAACTTCTCTGTGCAACCAATGGCTGTACAGACTGGGCTTCAGCT   | 699  |
| Db | 697  | ACAGTGTGGCAGGAAGAACTTCTCTGTGCAACCAATGGCTGTACAGACTGGGCTTCAGCT   | 756  |
| QY | 700  | TCTCGAGATTTTGTCCATCAGCTGGGAGATTTCACTGTTATTTGTTCATCGTGGCA       | 759  |
| Db | 757  | TCTCGAGATTTTGTCCATCAGCTGGGAGATTTCACTGTTATTTGTTCATCGTGGCA       | 816  |
| QY | 760  | TGGGCGAGATTCGCAACTATGATGATGATCCTTATATCTAGAGACAGAAATTTCTGGCAAT  | 819  |
| Db | 817  | TGGGCGAGATTCGCAACTATGATGATGATCCTTATATCTAGAGACAGAAATTTCTGGCAAT  | 876  |
| QY | 820  | CAGTTTCGATTTATTTCTCTACATTTAGAGAGTGTGCACATTTTTCAGATGGCTATATGC   | 879  |
| Db | 877  | CAGTTTCGATTTATTTCTCTACATTTAGAGAGTGTGCATATTTTATGATTTGGCTATATGG  | 936  |
| QY | 880  | TGCTGCCACTGTTTGTCTTACTATCAGAGAGCTGGCGGATGCTGCTGGCGCTGACGG      | 939  |
| Db | 937  | TGCTGCCACTGTTTGTCTTACTATCAGAGAGCTGGCGGATGCTGCTGGCGCTGACGA      | 996  |
| QY | 940  | TGCGGGAGTGTGTGTGTCGCCGCTGGGTGTGTTATTCCTGAAATCTCCCGATGGCTGA     | 999  |
| Db | 997  | TGCGGGAGTGTGTGTGTCGCCGCTGGGTGTGTTATTCCTGAAATCTCCCGATGGCTGA     | 1054 |
| QY | 1000 | TATCCAGAGAAAGATTTAGAGAGGCTGAAGATATCATCCAAAAGCTGCAAAAATGAGACA   | 1055 |
| Db | 1057 | TCTCTCAGAGGAGATTTAGAGAGGCGAGAGGATATCATCCGCAAGGCTGCAAAAATGAG    | 1111 |
| QY | 1060 | ACACAGCTGTACACAGATGATTTGATTCGTGGAG-----GAGCTAAATCCCCCTGA       | 1117 |
| Db | 1117 | GGATTTGTGTGCTTCCACTATCTTTTGACCCGAGTGAAGATTCACAAACCTCAATCTCCAGA | 1174 |
| QY | 1114 | AGCAGCAGAAAGCTTTCATCTGTGAGACCTGTTACAGACTCGGAAATTTGCCATTAATGACA | 1177 |
| Db | 1177 | AGCAGCAGATTCOAACAACTGTGATTCGTGCTTCGAACTGGAAATTCGCGAATGGTACCA   | 1233 |
| QY | 1174 | TTATGTCCTTGTCTGTATGATGCTGACCTCAGTGGGTAACTTGTCTGTCTGTGATG       | 1233 |
| Db | 1237 | TCATGTCATATATGCTGTGATGACCAATATAGTGGGCTATTTTGGGCTTGTGCTTGAATA   | 1299 |

| Accession | Sequence   | Length |
|-----------|--|--------|
| U7        | AGCAGCACAAGGCTTTTCTTCTGGAGCCGTTTCAGGACATCGGAAATTTGGCAATAAAGACA     | 117    |
| Db        | 1177 AGCAGCATTCCCAACAACATCTGGATCTGCTTCGAACTGGAAATTCGGAGATGTCACACA  | 123    |
| QY        | 1174 TTATGCTTTTGCTGCTATGAGATCGTACGACTAGTGGGTAACTTTGCTCTGTCTGTGATG  | 123    |
| Db        | 1237 TCATGTCATATATGCTGTGGATGACCAATATAGTGGGCTATTTTGGGCTTTGCGTTGATTA | 129    |



|    |      |   |      |
|----|------|---|------|
| QY | 1354 | AGTACGCTGTGGGGAGGAGAGTGCTGCTTCATTCACATGGTACTGGGATTAAT             | 1413 |
| Db | 1417 | CTGGCCCTCTCTGGGGGAGAGTGTCTCTTCATGACAGCTGGATCCCACTGT               | 1476 |
| QY | 1414 | ACTTCCTATCATGTGCTGTGCATGCTGGGAAAATTGGGATCACTGCTTCTCCA             | 1473 |
| Db | 1477 | ATTATTGGGCTACAGTCTGGTGTATGGTGGGCAAGTTGGATGACGGCTGCTTCCA           | 1536 |
| QY | 1474 | TGCTGTATGCTTCTACTGCTGAGCTCTAACCAACCTGGGTGACAGAAATGGCGTGGGG        | 1533 |
| Db | 1537 | TGGCTACAGTGTACACAGCCGAGCGTGTATCCACAGTGGTGAGAAACATGGGTGTGGAG       | 1596 |
| QY | 1534 | TCATATCCACGGCCCTCCAGATGGGGACACATCATGCCCCCTACTTGTATTACCTGGTG       | 1593 |
| Db | 1597 | TCACCTCCACAGCATCCCGCCTGGGGACACATCTGTCTCCCTACTTGTATTACCTGGTG       | 1656 |
| QY | 1594 | CTTACACAGAAATGCTGCCCTACATACGATGGGTAGTCTGACTGCTGATTTGGAAATCT       | 1653 |
| Db | 1657 | CTTACAGACCGTCTCTGCTGCTTACATTTCTCATATGGAAAGTCTGACCATCTCTGACACCATCC | 1716 |
| QY | 1654 | TCACCCCTTTTTTCCCTGGAAAAGTTGGGAATGACTCTTCCAGAAAACCTTGAAGACAGATGC   | 1713 |
| Db | 1717 | TCACCTGTGTTCTCCAGAGAGCTTGGTACCCCCACTCCAGACACCATTTGACAGATGC        | 1776 |
| QY | 1714 | AGAAAGTGAATGTTGTCAGATCTGGGAAAAAACAAGAGCTCAATGGAGACAGAAGAA         | 1773 |
| Db | 1777 | TAAAGATCAAAAGGAATGAACACAGAAAAACTCTCAAGTCCACACAAAGATGTTTAAAGAATG   | 1836 |
| QY | 1774 | ATC 1776  |      |
| Db | 1837 | GTC 1839  |      |

RESULT 11  
US-60-453-135-4827  
; Sequence 4827, Application US/60453135  
; GENERAL INFORMATION:  
; APPLICANT: CARGILU, Michele  
; APPLICANT: IAKOUBOVA, Olga  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001456  
; CURRENT APPLICATION NUMBER: US/60/453,135  
; CURRENT FILING DATE: 2003-03-10  
; NUMBER OF SEQ ID NOS: 82762  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4827  
; LENGTH: 3223  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-60-453-135-4827

Db 1477 ATATTGGCTACAGTCTGGTGTGATGGTGGCAAGTTTGGAGTCACAGCGTGCCTTTTCCA 1536  
OY 1474 TGGCTGATGCTTACTGCTGAGCTCTACCCAAACCCGTGTCAGAGAACTGGCGTGGGG 1533  
Db 1537 TGTCTGAGTGTACACAGCCAGCTGTATCCCAAGAGTGAAGAAATGGGTGGGAG 1596  
OY 1534 TCACATCCAGCGGCTCCAGAGTGGGAGCATCATTTGCCCCCTACTTGTGTACTCTGGT 1593  
Db 1597 TCACCTGACAGCATCCCGGCTGGGAGCATCCCTGTCTCTCTACTTGTGTACTCTGGT 1556  
OY 1594 CTTCACACAGATCT 1653  
Db 1657 CTTACGAGCGCT 1716  
OY 1654 TCACCT 1713  
Db 1717 TCACCTGTTCT 1776  
OY 1714 AGAAAGTGAATGTTTCT 1773  
Db 1777 TAAAGTCAAGAAAGTGAATGAACAGAAACCTCAAGTACACAGAGATGTAAAGATG 1836  
OY 1774 ATC 1776  
Db 1837 GTC 1839

RESULT 12  
US-60-453-050-4827  
: Sequence 4827, Application US/60453050  
: GENERAL INFORMATION:  
: APPLICANT: CARLILL, Michele  
: APPLICANT: LOKE, May  
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
: TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF  
: FILE REFERENCE: C1001457  
: CURRENT APPLICATION NUMBER: US/60/453,050  
: NUMBER OF SEQ ID NOS: 82762  
: SOFTWARE: FASTSEQ for Windows Version 4.0  
: SEQ ID NO 4827  
: LENGTH: 3223  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
US-60-453-050-4827

Query Match 47.68; Score 1016.2; DB 18; Length 3223;  
Best Local Similarity 75.68; Pred. No. 1.6e-232;  
Matches 1272; Conservative 17; Mismatches 370; Indels 24; Gaps 2;

OY 100 CGCTGTCATACCCGTAAGTTTGGAGCGGAGTGGAGAACATGCGGACTAGC 159  
Db 175 CGGGTTCGCGACCCGAGCGCGCTCTGTGGGCTCTGAGGGCGGAGTGGGACTAGC 234  
OY 160 ACGAGGTATCGCTTCTGGGGAGTGGGGGCGCTTCCAGGCGCTCATCTTCTCTGCG 219  
Db 235 ACGAGGTATCGCTTCTGGGGAGTGGGGGCGCTTCCAGGCGCTCATCTTCTCTGCG 294  
OY 220 TCAGCGCAGCATATCCCAATGAGTGTATGTCAGTGTGAGTGTCTCTGCGGAGG 279  
Db 295 TCAGCGCAGCATATCCCAATGAGTGTATGTCAGTGTGAGTGTCTCTGCGGAGG 354  
OY 280 CCGCGAGACCGCTCTCGAGTCCGAGCGCGGAGACTGAGACAGCGGCTGGCGAC 339  
Db 355 CCGCGAGACCGCTCTCGAGTCCGAGCGCGGAGACTGAGACAGCGGCTGGCGAC 414  
OY 340 ACAGTGTCCGCTGGGGAGTGGGGAGGCGGAGGTGCGGAGCTGACAGCTGACCGCTAC 399  
Db 415 ACAGTGTCCGCTGGGGAGTGGGGAGGCGGAGGTGCGGAGCTGACAGCTGACCGCTAC 474  
OY 400 GGGTCCACCATCGCAATCTCTGCGGCTGCGGCTGAGGCGGGGCGAGCTGAGAC 459

Db 475 GGGTCCACCATCGCAATCTCTGCGGCTGCGGCTGAGGCGGGGCGGAGCTGAGAC 534  
OY 460 TGGGGAGCTGGAGACAGAGAGACTGCTGGATGCTGGAGTTTCAGCCAGAGCTTACC 519  
Db 535 TGGGGAGCTGGAGACAGAGAGACTGCTGGATGCTGGAGTTTCAGCCAGAGCTTACC 594  
OY 520 TGTCCACGCTGACCGAGTGGAACTGTGTGTGAGGACAACTGGAAGGCGCCCTCA 579  
Db 595 TGTCCACGCTGACCGAGTGGAACTGTGTGTGAGGACAACTGGAAGGCGCCCTCA 636  
OY 580 CCACCTCCCTGTTCTGTAGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 639  
Db 637 CAATCT 696  
OY 640 ACAGGTTGGGAGGAAAGCTTCT 699  
Db 697 ACAGGTTGGGAGGAAAGCTTCT 756  
OY 700 TCTTCAGATTTCT 759  
Db 757 TCTTCAGATTTCT 816  
OY 760 TGGGCGAGATCTCCAACTATGTGTAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 819  
Db 817 TGGGCGAGATCTCCAACTATGTGTAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 876  
OY 820 CAGTTCGATATATTTCT 879  
Db 877 CAGTTCGATATATTTCT 936  
OY 880 TGTCTCCACGCTTGTCTTACTTCT 939  
Db 937 TGTCTCCACGCTTGTCTTACTTCT 996  
OY 940 TGGCGGAGTGTGTGTCT 999  
Db 997 TGGCGGAGTGTGTGTCT 1056  
OY 1000 TATCCAGAGAGATTTAGAGAGCTGAGATATCATCAAAAGCTGCAAAATTTGAGACA 1059  
Db 1057 TCTCTCAGGAGAGATTTGAGAGGAGAGGATGATCATCGGAAGGCTGCAAAATTTGAGACA 1116  
OY 1060 ACACAGCTGTACAGCACTGATATTTGATTTCTGTGGAG-----GAGCTAAATCCCTGA 1113  
Db 1117 GATGTTGTGTGCTTCCACTATCTTTGACCGAGAGATTTACAGCACTGATTTCCAGAGA 1176  
OY 1114 AGCAGCAGAAAGCTTTCATCTCTGAGCTGAGAGCTGAGAGCTGAGATTTGCAATTTAGACA 1173  
Db 1177 AGCAGCAGTCCCAACAATTTGATGATCTGTCTTCCAGCTGAGATTTGCAATTTAGACA 1236  
OY 1174 TTATGCTTTCTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1233  
Db 1237 TCATGTCATATATGT 1296  
OY 1234 CTCTCAATTTACATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1293  
Db 1297 CTCTCAATTTACATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1356  
OY 1294 CAGCTTACATTAACAGCTGCTGCTATGATGATGATGATGATGATGATGATGATGATGATGATG 1353  
Db 1357 CAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1416  
OY 1354 CAGTACTGTTCTGGGGAGAGGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1413  
Db 1417 CTGCGCTTCTCTGGGGAGAGGTGTCT 1476  
OY 1414 ACTTCTTATCCATGTTGT 1473  
Db 1477 ATATTGGCTACAGTCTGGTGTGATGGGCAAGTTTGGAGTCAACGCGCTGCTTTTCCA 1536  
OY 1474 TGGCTGATGCTTACTGCTGAGCTTACCAACCCGTGTCAGAGAACTGGCGTGGGG 1533  
Db 1537 TGTCTGAGTGTACACAGCCAGCTGTATCCCAAGAGTGAAGAAATGGGTGGGAG 1596

|    |      |  |      |
|----|------|--|------|
| OY | 1534 | TCACATCCAGGGCCTCCAGAGTGGGAGCATCAATTGCCCCCTACTTTGTTACTCGGTG   | 1593 |
| Db | 1597 | TCACTCTCACAGCATCCCGCTGGGAGCATCTGTCTCTACTTTGGTTAACTTTGGTG     | 1656 |
| OY | 1594 | CTTACACACAGAATCTGCCTTACATTCGTATGGGTAGTCTGCATGTCCCTGATTGAATCT | 1653 |
| Db | 1657 | CCTACGACCGCTTCTCCTCCCTACATTTCTCATGGSAATCTGACCATCTGACACCCATTC | 1716 |
| OY | 1654 | TCACCCTTTTTTCCTTGAAAATTGSGAATGACTCTTCCAGAAACCTTAGAGCAGATGC   | 1713 |
| Db | 1717 | TCACCTGTTTCTCCAGAGAGCTTCGTTACCCCACTCCAGACACCATATGCCAGATGTC   | 1776 |
| OY | 1714 | AGAAAGTGAATGGTTTCAGATCTGTGGAAAAAACAGAGCATCAATGAGAGACAGAAAA   | 1773 |
| Db | 1777 | TAAAGTCAAAGGAATGAACACAGAAAAAATCCAAAGTCACACAAGATGTTTAAAGATG   | 1836 |
| OY | 1774 | ATC 1776   |      |
| Db | 1837 | GTC 1839   |      |

```

RESULT 13
US-60-466-412-4827
: Sequence 4827, Application US/60466412
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele
: APPLICANT: IAKOUBOVA, Olga
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001466
: CURRENT APPLICATION NUMBER: US/60/466,412
: CURRENT FILING DATE: 2003-04-30
: NUMBER OF SEQ ID NOS: 429241
: SOFTWARE: FASTSEQ For Windows Version 4.0
: SEQ ID NO 4827
: LENGTH: 3223
: TYPE: DNA
: ORGANISM: Homo sapiens
US-60-466-412-4827

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| Query Match           | 47.6%  | Score 1016.2       | DB 19     | Length 3223 |
|-----------------------|--|--------------------|-----------|-------------|
| Best Local Similarity | 75.6%  | Pred. No. 1.6e-232 |           |             |
| Matches 1272          | Conservative 17  | Mismatches 370     | Indels 24 | Gaps 2      |
| QY                    | CGCTGTCAATCAACCCGATGTCACAAATTTCGGAGCGGCGAGTGGGAGATCGGGGACTACG        | 159                |           |             |
| DB                    | 175 GCGGTCCCMAGACCCCGAGCGCGCGCTCTGTGGCGCTCTGAGGGCGGCGATTCGGGAGCTACG  | 234                |           |             |
| QY                    | 160 ACGAGGTATGCGCTTCTCTGGGCGAGTGGGGGCGCTTCAGCGGCTCATCTCTTCCTGCG      | 219                |           |             |
| DB                    | 235 ACGAGGTATGCGGCTTCTCTGGGCGAGTGGGGGCGCTTCAGCGGCTCATCTCTTCCTGCG     | 294                |           |             |
| QY                    | 220 TCAGGGCGAGATCATTCGCCCAATGGCTCAATGATGATTCAGTTCAGTTCGTTCCTGCGGGGGA | 279                |           |             |
| DB                    | 235 TCAGGGCGAGATCATTCGCCCAATGGCTTCACCGGCGCTGTCTCTCGGTCTCTGATAGCGA    | 354                |           |             |
| QY                    | 280 CCGCGGAGCACCGCTGTGAGTGGCGGAGCGCGCGCAACCTGACGACGCGCTGGCGCAACA     | 339                |           |             |
| DB                    | 355 CCGCGGAGCACCGCTGTGAGTGGCGGAGCGCGCGCAACCTGAGCAGCGCTGGCGCAACC      | 414                |           |             |
| QY                    | 340 ACAGTGTCCCGTGGGGGCTGGGGGAGCGGCGGGAAGTCCCCACAGCTTCGACGCCGCTAC     | 399                |           |             |
| DB                    | 415 ACAGTGTCCCACTGGGGTGGGGGAGCGGCGGGAAGTCCCCACAGCTTCGCGCCGCTAC       | 474                |           |             |
| QY                    | 400 GCGTGGCACCATCGCAACTTCTGGGGCTGGGGCTGAGCGCGGGGGCGGCGACTGGGAC       | 459                |           |             |
| DB                    | 475 GCGTGGCACCATTCGCAACTTCTGGGGCTGGGGCTGAGAGCGCGGGGGCGGAGCGTGGAC     | 534                |           |             |
| QY                    | 460 TGGGGCAGCTGGAGCAGGAGAGCGCTCTGATGCTGGGAGTTACACCGACGAGCGTCTAC      | 519                |           |             |
| DB                    | 535 TGGGGCAGCTGGAGCAGGAGAGCGCTCTGATGCTGGGAGTTACAGTCAGGAGCGTCTAC      | 594                |           |             |

|    |      |  |      |
|----|------|--|------|
| QY | 520  | TGTCACACCCTGTCACCGAGTGGAAATCGTGTGTGTATGAGCAACACTGGAAAGTCCCTCTCA  | 579  |
|    |      |  |      |
|    |      |  |      |
| Db | 595  | TGTCACACATTTGTATACC-----GAGGACGACTGGAAAGCCCCCACTCA               | 636  |
|    |      |  |      |
| QY | 580  | CCACCTCCCTGTTTCTTGATGAGCGCTGCTCCCGACTCTTCATGCTCCGGGACACTGTCA     | 639  |
|    |      |  |      |
|    |      |  |      |
| Db | 637  | CANCTCTCTTGTCTTGTGTGGGTGCTGTGTGGCTCTTCATTTTCAAGGGACACTGTCA       | 696  |
|    |      |  |      |
| QY | 640  | ACAGTTTGGCAGGAAGAACGTTCTCTCGCAACCATGGCTGTACAGACTGGCTTCAGCT       | 699  |
|    |      |  |      |
| Db | 697  | ACAGTTTGGCGTGAAGAAATGCTGTTTCGACCATGGCCATGCAACAGCGCTTCAGCT        | 756  |
|    |      |  |      |
| QY | 700  | TCTCGCAGATTTTCTCATCAGCTGGGAGAGATGTCACATGTTATTTGATATGTTGGGCA      | 759  |
|    |      |  |      |
| Db | 757  | TCTCGCAGATCTCTCGAAGATTTTGAAGATGTTGTGTGTGCTGTGTGTCTTGTCTGTGAGCA   | 816  |
|    |      |  |      |
| QY | 760  | TGGGCCAGATCTCCACATATGTGGTAGCTTCATCTACACAGAAATTTCTTGGCAAGT        | 819  |
|    |      |  |      |
| Db | 817  | TGGGCCAGATCTCCACATCTGTGGCAGCATTTGTCCTGGGGACAGAAATTTCTTGGCAAGT    | 876  |
|    |      |  |      |
| QY | 820  | CAGTTTCGTATTAATTTCTCTACATTAGGAGTGTGCACATTTTGTGCAAGTTGGCTATATGC   | 879  |
|    |      |  |      |
| Db | 877  | CAGTTTCGTATTAATTTCTCTACAGTTAGAGTGTGCATATTTTATGCAATTTTGKCTACATGCG | 936  |
|    |      |  |      |
| QY | 880  | TGCTGCCCTGTTTGGCTTACTTTCATCTACACAGAGCTGGCGAATGCTCTCTGGCGCTGACGG  | 939  |
|    |      |  |      |
| Db | 937  | TGCTGCCCTGTTTGGCTTACTTTCATCTACACAGAGCTGGCGAATGCTCTCTGGCGCTGACGG  | 996  |
|    |      |  |      |
| QY | 940  | TGCGGGAGTCTGTGTGTCTCCGCTGTGTGTGTTCAATTCCTGAATCTCCCGATGCTCA       | 999  |
|    |      |  |      |
| Db | 997  | TGCGGGAGTCTGTGTGTCTCCGCTGTGTGTGTTCAATTCCTGAATCTCCCGATGCTCA       | 1056 |
|    |      |  |      |
| QY | 1000 | TATCCACAGAGAATTTTGAAGAGCTGGAATATCATCCAAAGACTGCAGAAATATGACA       | 1059 |
|    |      |  |      |
| Db | 1057 | TCTCTCAGGAGCAGATTTTGAAGAGCAGAGTGATCATCCGCAAGGCTGCMCAAGCCATG      | 1116 |
|    |      |  |      |
| QY | 1060 | AACACAGCTGTACACAGCACTGATATTGTATTTCTGTGAG-----GAGCTAAATCCCTGA     | 1113 |
|    |      |  |      |
| Db | 1117 | GGATTTGTGTGCTCTCCACTATCTTTTGGACCGAGATGAGTTCAAGACTTAAGTTCCAGA     | 1176 |
|    |      |  |      |
| QY | 1114 | AGCAGCAAGAAAGCTTTCATTTCTGACACCTGTGACAGACTCGGGAATATGCCATATGACA    | 1173 |
|    |      |  |      |
| Db | 1177 | AGCAGCAATCCCAACAACATTTGATGTGCTGTTCGAACTGGAAATATCCGATGTGTACCA     | 1236 |
|    |      |  |      |
| QY | 1174 | TTATGTCTTGTCTGTATGATGTCAGCTCAAGTGGGTACTTGTCTGTCTGTCTGTGATG       | 1233 |
|    |      |  |      |
| Db | 1237 | TCATGTCCATATATGCTGTGTGATGACCATATATCAGTGGGCAATTTTGGGCTTCCGCTGATA  | 1296 |
|    |      |  |      |
| QY | 1234 | CTCTTAATTTACATGAGATGCTTACCTGGAAGTGTTCCTCTGTCTGTGTATTTGAATTC      | 1293 |
|    |      |  |      |
| Db | 1297 | CTCTTAATTTACATGAGATGCTTACCTGGAAGTGTTCCTCTGTGTATTTGAATTC          | 1356 |
|    |      |  |      |
| QY | 1294 | CAGCTTACATTTACACCTGTGGCTGTATTTGCAACAGCTCCCAAGCGTATATCTATAGCTG    | 1353 |
|    |      |  |      |
| Db | 1357 | CAGCATATGTGTGGCTGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT     | 1416 |
|    |      |  |      |
| QY | 1354 | CAGTACTGTTCTGGGAGAGAGGTGTGCTTCTCTTCAATTCAGTGTACTGTGTATTTT        | 1413 |
|    |      |  |      |
| Db | 1417 | CTGCCCTCTCTCTGGGTGGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT   | 1476 |
|    |      |  |      |
| QY | 1414 | ACTCTTATTTACCTGCTGTGGT     | 1473 |
|    |      |  |      |
| Db | 1477 | ATTATTTGGCTTACATGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT      | 1538 |
|    |      |  |      |
| QY | 1474 | TGCTGTATGTCTTCACTGTGATCTGTACCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 1533 |
|    |      |  |      |
| Db | 1537 | TGCTGTATGTCTTCACTGTGATCTGTACCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 1596 |
|    |      |  |      |
| QY | 1534 | TGCTGTATGTCTTCACTGTGATCTGTACCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 1593 |
|    |      |  |      |
| Db | 1597 | TGCTGTATGTCTTCACTGTGATCTGTACCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT   | 1656 |
|    |      |  |      |
| QY | 1594 | CTTAAACAGATGTGTGCTTCACTGTGATCTGTACCCAACTGTGTGTGTGTGTGTGTGTGTGTGT | 1653 |
|    |      |  |      |

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Db      1657 CCTAGACGCGCTTCTGCTGCTTACATCTCATGGGAGCTGACCATCTGACAGCCATCC 1716
QY      1654 TCACCTTTTTCCTGAAAGTTGGGAATGACTTTCAGAAACCTTGAGAGATGC 1713
Db      1717 TCACCTGTTTCTCCAGAGAGCTTCGATCCCACTCCAGACACCATGACAGATGC 1776
QY      1714 AGAAATGAAATGTTGATCTGGGAAAAAACACAGAGATCAATGAGACAGAGAAA 1773
Db      1777 TAAGAGTCAAGAGATGAAACACAGAAAACTCAAGTACACAGAGATGTTAAAGATG 1836
QY      1774 ATC 1776
Db      1837 GTC 1839

RESULT 14
US-10-144-771-9977
; Sequence 9977, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 9977
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: HUMAN
US-10-144-771-9977

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Query Match      46.6%; Score 994; DB 14; Length 2574;
Best Local Similarity 75.7%; Pred. No. 3e-227;
Matches 1247; Conservative 0; Mismatches 395; Indels 6; Gaps 1;

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QY      130 GAGGCGAGTGGGAGAGCATGCGGAGCTACAGACAGAGTGAATCCGCTTCGAGGATGGG 189
Db      99 GGGAGGCTGAGAGAGCGCATCGGAGCTACAGACAGAGTGAATCCGCTTCGAGGATGGG 158
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Db      159 GGGCCCTTCAGCGCCTCATCTTCTCTGCTCAGCGCCAGCATCATCCCAATGGCTTCA 218
QY      250 ATGATATGTAGTGTGTTCTGTTGGGGGAGCCCGAGAGACGCGTGTGAGTCCGAGC 309
Db      219 ATGATATGTAGTGTGTTCTGTTGGGGGAGCCCGAGAGACGCGTGTGAGTCCGAGC 278
QY      310 CCGGAGACTGAGCAGCGGCTGGGCAACAACAGTGTCCGCTGGCGGCTGGGAGCGCC 369
Db      279 CCGTGAACCTGAGCAGCGGCTGGGCAACAACAGTGTCCGCTGGGAGCGGAGCGCC 338
QY      370 GCGAGGTGCCCAAGCTGAGCGGCTACCGGCTCGCCACATCCGCAACTTCTGGCGC 429
Db      339 GACAGGTGCCCTCAGAAATGCGCGGCTACCGGCTCGCCACATCCGCAACTTCTGGAGC 398
QY      430 TCGGCGTGGAGCGGGGCGCGAGCTGAGCTGGGCGAGCTGAGAGAGAGAGCTGGC 489
Db      399 TAGGCGTGGAGCGGGGCGCGAGCTGAGCTGGGCGAGCTGAGAGAGAGAGCTGGC 458
QY      490 ATGCTGGGAGTTCAACGAGAGAGTGTACTCTGTCACCGTGGTGAACCGGAGGAGATCG 549
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QY      550 TGTGTGAGAGCAACTGGAAGGTGCCCTCACACCTCTCTGTTCTTCGTAGCGGTGCC 609
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QY      610 TGGGCTCTTCTGTTCTGGGCGAGCTGTACAGAGGTTTGGCAGAGAGAGCTTCTCTGC 669
Db      579 TGGGCTCTTCTGTTCTGGGCGAGCTGTACAGAGGTTTGGCAGAGAGATGTCTTCTT 638
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Db      639 TGACCATGGGAGATGAGAGCTGAGCTTCTGAGAGTCTTCTCTGGAACCTTCGAGA 698
QY      730 TGTTCACCTGTATTATTTGATCGTGGGATGGGATGGGATGCAACTATGTAGTGCCT 789
Db      699 TGTTCACCTGTATTATTTGATCGTGGGATGGGATGGGATGCAACTATGTAGTGCCT 758
QY      790 TCATATGAGACAGAAATCTTGGCAGTGGTGTGATTTATTTCTCTCATATGAG 849
Db      759 TGTCTGGGAAACAGAAATCTTTCATGATTTGATTTATTTGCGCACTTAGAG 818
QY      850 TGTGACATTTTTCGAGTTGGCTATATGCTGTCCCACTGTTCCTACTTATCATCAGAG 909
Db      819 TTTGATATTTATGAGTTTGGCTTTCATATGCTGTCCCACTGTTCATATCATCAGAG 878
QY      910 ACTGGCGATGCTGCTGCTGGGCGTACAGGATGGGAGTGTGTGTCTCCGCTGTGCT 969
Db      879 ACTGGAGGATGCTGCTGCTGGGCGTACAGGATGGGAGTGTGTGTCTCCGCTGTGCT 938
QY      970 GGTTCATTCCTGAATCTCCCGATGCGATATGCCAGAGAAATTTAGAGAGCTGAG 1029
Db      939 GGTTCATTCCTGATGCTCCAGATGCGATATGCCAGAGAAATTTAGAGAGCTGAG 998
QY      1030 ATATCATCCAAAAGCTGCAAAATGAACACACAGCTGTACACAGCTGATATTTGAT 1089
Db      999 TGATCATCCGCAAAAGCTGCAAAATGAACAGGATTTGACACTTCACATATCTGATC 1058
QY      1090 CTGTGAG-----GAGCTAAATCCCTGGAAGCAGACAAAGCTTTATTTGACACTGT 1143
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QY      1144 TCAGAGACTGCAATATGTCATATGATGACCATATGCTTCTGCTGATGATGATGACCT 1203
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QY      1264 ACTGTTCTCTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1323
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QY      1334 GAACGCTGCCAGGCGTTATATCATAGCTGAGTACTGTTGGGAGAGAGTGTGCTTC 1383
Db      1299 AGTACTGCCCCGGGATATCTATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1358
QY      1384 TCTTATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1443
Db      1359 TCTTATTCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1418
QY      1444 GAAATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1503
Db      1419 GAAATTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1478
QY      1504 CAACCTGCTGAGAAATGAGGAGTGGGAGTGCATCCAGGCTCCAGAGTGGGAGCA 1563
Db      1479 CCACCTGCTGAGAAATGAGGAGTGGGAGTGCATCCAGGCTCCAGAGTGGGAGCA 1538
QY      1564 TCATTTGCCCCCTACTTGTGTTTACTCGGTGTTCAACAGAGTGTCTCTTACATGCTCA 1623
Db      1539 TCTGCTGCTCCCTACTTGTGTTTACTCGGTGTTCAACAGAGTGTCTCTTACATGCTCA 1598
QY      1624 TGGTATGCTGAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1683
Db      1599 TGGGAGTGTACCATCTCTGAGCTATCTCTACCTTGTCTTCTCTGAGAGCTTGTG 1658
QY      1684 TGACTCTTCAGAAACCTTACAGAGATGAGAGAAATGTTTCAATCTGAGAGAA 1743
Db      1659 TCCCTTCGCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1718
QY      1744 AAACAGAGACTCAATGAGAGAGAA 1771

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Db      1464  CCACTGTGTGACAGAAACATGGGTGTGGGGGTCACTCCACAGCATCCCGCTTGGCAGCA 1523
QY      1564  TCATGGCCCCCTACTTGTGTACCTGGGTCTTACAACAGAAATGCTGCCCTACATGTCA 1623
Db      1524  TCCGTCTCCCTACTTGTCTACCTTGGTGCCTATGATCGCTTCCTGCTTATATCTCA 1583
QY      1624  TGGGTAGTCTGACTGTCTGATTGGAATCTTACCCCTTTTCCCTGAAAGTTGGAA 1683
Db      1584  TGGGAAGCTGTACCATCTGTACAGCTATCTCTACCTTGTCTTCCAGAGAGCTTGTG 1643
QY      1684  TGACTCTTCCAGAAACCTTAGAGCAGATGCAAGATGAATGTTAGATCTGGGAAA 1743
Db      1644  CCCCTCTCCCGACACCATGTGACGATGCTCAGGGTCAAAAGGATATAAACAATGGCAA 1703
QY      1744  AAACAAGAGCTCATGTGAGACAGAAAG 1771
Db      1704  TCCAAAGCCAAACAGAGACGCAAAAGA 1731
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Search completed: July 5, 2003, 08:54:51  
Job time : 1590 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2003, 12:29:59 ; Search time 18 Seconds  
(without alignments)  
900.668 Million cell updates/sec

Title: US-09-521-195B-1

Perfect score: 2845  
Sequence: 1 MKDDEVIAFLGEMGFQRL.....KTRDSMETENPKVLTAF 551

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCtus.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID               | Description        |
|------------|-------|-------------|--------|------------------|--------------------|
| 1          | 702   | 24.7        | 555    | US-08-501-572-3  | Sequence 3, Appli  |
| 2          | 702   | 24.7        | 555    | US-09-040-444-3  | Sequence 3, Appli  |
| 3          | 687.5 | 24.2        | 556    | US-08-501-572-1  | Sequence 1, Appli  |
| 4          | 687.5 | 24.2        | 556    | US-09-040-444-1  | Sequence 1, Appli  |
| 5          | 680   | 23.9        | 553    | US-08-501-572-2  | Sequence 2, Appli  |
| 6          | 680   | 23.9        | 553    | US-09-040-444-2  | Sequence 2, Appli  |
| 7          | 630   | 22.1        | 537    | US-08-647-397-2  | Sequence 2, Appli  |
| 8          | 606.5 | 21.3        | 545    | US-09-572-147-2  | Sequence 2, Appli  |
| 9          | 586   | 20.6        | 550    | US-09-330-245A-2 | Sequence 2, Appli  |
| 10         | 267   | 9.4         | 520    | US-08-964-127-2  | Sequence 2, Appli  |
| 11         | 267   | 9.4         | 520    | US-09-496-692-2  | Sequence 2, Appli  |
| 12         | 234.5 | 8.2         | 494    | US-09-031-392-5  | Sequence 5, Appli  |
| 13         | 234.5 | 8.2         | 494    | US-09-299-549-5  | Sequence 5, Appli  |
| 14         | 234.5 | 8.2         | 494    | US-09-610-417-5  | Sequence 5, Appli  |
| 15         | 222   | 7.8         | 492    | US-08-355-844-3  | Sequence 5, Appli  |
| 16         | 222   | 7.8         | 492    | PCT-US95-16126-3 | Sequence 3, Appli  |
| 17         | 216   | 7.6         | 493    | US-09-031-392-10 | Sequence 10, Appli |
| 18         | 216   | 7.6         | 493    | US-09-299-549-10 | Sequence 10, Appli |
| 19         | 216   | 7.6         | 493    | US-09-610-417-10 | Sequence 10, Appli |
| 20         | 216   | 7.6         | 510    | US-09-291-922-22 | Sequence 22, Appli |
| 21         | 213.5 | 7.5         | 524    | US-08-928-692-12 | Sequence 12, Appli |
| 22         | 213.5 | 7.5         | 524    | US-09-339-972-12 | Sequence 12, Appli |
| 23         | 213.5 | 7.5         | 529    | US-09-291-922-28 | Sequence 28, Appli |
| 24         | 206.5 | 7.3         | 549    | US-09-291-922-30 | Sequence 30, Appli |
| 25         | 204.5 | 7.2         | 539    | US-09-291-922-26 | Sequence 26, Appli |
| 26         | 203   | 7.1         | 286    | US-08-964-127-4  | Sequence 4, Appli  |
| 27         | 203   | 7.1         | 286    | US-09-496-692-4  | Sequence 4, Appli  |

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| 28 | 196   | 6.9 | 323 | US-09-134-001C-4635 | Sequence 4635, Ap  |
| 29 | 196   | 6.9 | 500 | US-09-031-392-7     | Sequence 7, Appli  |
| 30 | 196   | 6.9 | 500 | US-08-299-549-7     | Sequence 7, Appli  |
| 31 | 196   | 6.9 | 500 | US-09-610-417-7     | Sequence 7, Appli  |
| 32 | 194   | 6.8 | 513 | US-09-291-922-20    | Sequence 20, Appli |
| 33 | 188.5 | 6.6 | 523 | US-09-291-922-24    | Sequence 24, Appli |
| 34 | 181   | 6.4 | 509 | US-09-031-392-6     | Sequence 6, Appli  |
| 35 | 181   | 6.4 | 509 | US-09-299-549-6     | Sequence 6, Appli  |
| 36 | 181   | 6.4 | 509 | US-09-610-417-6     | Sequence 6, Appli  |
| 37 | 174.5 | 6.1 | 584 | US-08-928-692-13    | Sequence 13, Appli |
| 38 | 174.5 | 6.1 | 584 | US-09-339-972-13    | Sequence 13, Appli |
| 39 | 172   | 6.0 | 383 | US-09-031-392-3     | Sequence 3, Appli  |
| 40 | 172   | 6.0 | 383 | US-09-299-549-3     | Sequence 3, Appli  |
| 41 | 172   | 6.0 | 383 | US-09-610-417-3     | Sequence 3, Appli  |
| 42 | 170.5 | 6.0 | 470 | US-09-134-001C-4610 | Sequence 4610, Ap  |
| 43 | 169.5 | 6.0 | 488 | US-08-928-692-11    | Sequence 11, Appli |
| 44 | 169.5 | 6.0 | 488 | US-09-339-972-11    | Sequence 11, Appli |
| 45 | 168.5 | 5.9 | 488 | US-08-928-692-10    | Sequence 10, Appli |

#### ALIGNMENTS

RESULT 1  
US-08-501-572-3  
Sequence 3, Application US/08501572

Patent No. 6063623

GENERAL INFORMATION:

APPLICANT: Koepsell, Hermann

APPLICANT: Grundeman, Dirk

APPLICANT: Gorboulev, Valentin

TITLE OF INVENTION: Transport protein which effects the

TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,

TITLE OF INVENTION: DNA Sequences Encoding It And Their Use.

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/501,572

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Toohey, Kimberlin M

REGISTRATION NUMBER: 35,391

REFERENCE/DOCKET NUMBER: 02481.1453-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 555 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-501-572-3

Query Match

Best Local Similarity 33.7%; Score 702; DB 3; Length 555;

Matches 187; Conservative 93; Mismatches 229; Indels 46; Gaps 14;

5 DEVIATFLGEMGFQRLIF---LTSATIPNGNGMSVFLACTPGRKVPDANTS--59

Db 6 DVLHGEHFHFOKMFLLALLSATFAP---IYGVIFLGFPPDRHCRSPGVAELSLR 62  
QY 60 SAMR-----NNSVPLRLDGRVPHSCRYRLA-TIANFSALGLEPGRVDLGOLEQESC 113  
Db 63 CGWSPAELNTYVPGPGPAGASPRQCRREYVDNMNSTPDCVDPLASLDTNRSRLPLGPC 122  
QY 114 LDGMEFSQDYYLSTVVTENMLVCEDNMKVPLTSLFEVGLSGFVSQGLSDRFGRKNVL 173  
Db 123 RDGMVY--ETPGSSIVTEFNLVCANSMMLDFQSSVNVGFEFGMSIGYIADRGRKLC 180  
QY 174 FATMAVQTFSEFLQISWEMFTVLFVYVGMQISNYVAFLGTEILKSVRIITSTL 233  
Db 181 LTTVLINMAAGVIMASPTTYMMLIFRLIOGLVSKAGWILGILITEFVGGRYR--RTV 237  
QY 234 GVC--TFFAVGYMLPLFAVFIKDMRMMLLALTPGVLCVPLMWFIPESPRMLISQRRFR 291  
Db 238 GIFYVAYTYGVLVAGVAVLPHRMWLOFTVALPFFLLTYWCIPESPRMLISQKNNA 297  
QY 292 EADITOKAKKNNNTAVPAVI-----FDSVEELNPLKQOKAFILDLEFRINIAIMTMS 345  
Db 298 EAMRIIKHAKKNGKSLPASLQRLLEETGKKLNP-----SFLDVRTPOIRKHTMIL 351  
QY 346 LLLMMLTVSGYFALSADAPNLHGD-AYNCLFSALIEIPAYITAMLLFTLPRRYITAAV 404  
Db 352 MYNMTSSVLYOGLIMHM-GLAGDNITYLDFEYSALVEFPAAFMILLIIRIGRIPMAAS 410  
QY 405 LFWGGVLLFIQLVPVDYFLSIGLVMKFGITSASFMLYFETAEIYPLVRNMAVGYT 464  
Db 411 NMVAGACLASVFIQDLOWLKTIISCLGRMGITMAYIVCLVNAELIYPTIRNLGVHIC 470  
QY 465 STASRVGSIAPFYVLYGAYNRM-----LPIYVMSLTVLIGIFLTFEPESLGMILPET 518  
Db 471 SSMCDIGGITPFLVY----RLTNIMLEPLMVGVLVAGLALLPETKGAALPET 525  
QY 519 LEOMQKVMFRSGK 533  
Db 526 IEEAENMOPRRKKE 540

RESULT 2  
US-09-040-444-3  
Sequence 3, Application US/09040444  
Patent No. 6063766  
GENERAL INFORMATION:  
APPLICANT: Koepsell, Hermann  
APPLICANT: Grundeman, Dirk  
APPLICANT: Gorboulev, Valentin  
TITLE OF INVENTION: Transport Protein Which Effects The  
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner, L.L.P.  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/040/444  
FILING DATE: March 18, 1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: O'Connor, Steven P  
REGISTRATION NUMBER: 41,225  
REFERENCE/DOCKET NUMBER: 2481.1453-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)408-4000

TELEFAX: (202)408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 555 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-040-444-3

Query Match 24.7%; Score 702; DB 3; Length 555;  
Best Local Similarity 33.7%; Pred. No. 9.9e-65;  
Matches 187; Conservative 93; Mismatches 229; Indels 46; Gaps 14;

QY 5 DEVIAFGEWGPQRLIFF---LISASITPNFGMSVFLAGPBEHRCRVPDANLS-- 59  
Db 6 DVLHGEHFHFOKMFLLALLSATFAP---IYGVIFLGFPPDRHCRSPGVAELSLR 62  
QY 60 SAMR-----NNSVPLRLDGRVPHSCRYRLA-TIANFSALGLEPGRVDLGOLEQESC 113  
Db 63 CGWSPAELNTYVPGPGPAGASPRQCRREYVDNMNSTPDCVDPLASLDTNRSRLPLGPC 122  
QY 114 LDGMEFSQDYYLSTVVTENMLVCEDNMKVPLTSLFEVGLSGFVSQGLSDRFGRKNVL 173  
Db 123 RDGMVY--ETPGSSIVTEFNLVCANSMMLDFQSSVNVGFEFGMSIGYIADRGRKLC 180  
QY 174 FATMAVQTFSEFLQISWEMFTVLFVYVGMQISNYVAFLGTEILKSVRIITSTL 233  
Db 181 LTTVLINMAAGVIMASPTTYMMLIFRLIOGLVSKAGWILGILITEFVGGRYR--RTV 237  
QY 234 GVC--TFFAVGYMLPLFAVFIKDMRMMLLALTPGVLCVPLMWFIPESPRMLISQRRFR 291  
Db 238 GIFYVAYTYGVLVAGVAVLPHRMWLOFTVALPFFLLTYWCIPESPRMLISQKNNA 297  
QY 292 EADITOKAKKNNNTAVPAVI-----FDSVEELNPLKQOKAFILDLEFRINIAIMTMS 345  
Db 298 EAMRIIKHAKKNGKSLPASLQRLLEETGKKLNP-----SFLDVRTPOIRKHTMIL 351  
QY 346 LLLMMLTVSGYFALSADAPNLHGD-AYNCLFSALIEIPAYITAMLLFTLPRRYITAAV 404  
Db 352 MYNMTSSVLYOGLIMHM-GLAGDNITYLDFEYSALVEFPAAFMILLIIRIGRIPMAAS 410  
QY 405 LFWGGVLLFIQLVPVDYFLSIGLVMKFGITSASFMLYFETAEIYPLVRNMAVGYT 464  
Db 411 NMVAGACLASVFIQDLOWLKTIISCLGRMGITMAYIVCLVNAELIYPTIRNLGVHIC 470  
QY 465 STASRVGSIAPFYVLYGAYNRM-----LPIYVMSLTVLIGIFLTFEPESLGMILPET 518  
Db 471 SSMCDIGGITPFLVY----RLTNIMLEPLMVGVLVAGLALLPETKGAALPET 525  
QY 519 LEOMQKVMFRSGK 533  
Db 526 IEEAENMOPRRKKE 540

RESULT 3  
US-08-501-572-1  
Sequence 1, Application US/08501572  
Patent No. 6063623  
GENERAL INFORMATION:  
APPLICANT: Koepsell, Hermann  
APPLICANT: Grundeman, Dirk  
APPLICANT: Gorboulev, Valentin  
TITLE OF INVENTION: Transport Protein Which Effects The  
TITLE OF INVENTION: Transport Of Cationic Xenobiotics and/or Pharmaceuticals,  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA





Query Match 23.9%; Score 680; DB 3; Length 553;  
 Best Local Similarity 33.4%; Pred. No. 2e-62; Indels 70; Gaps 15;  
 Matches 192; Conservative 85; Mismatches 228;

1 MRDYDVIAFLGEMGFQF---LIFPLSASIIIPNGFNGSVFLAGTPEHRCRPDAN 57  
 1 MPTVDILBQVSSGFQQAFLICLLSAFAP---ICVIGLFTDHHQSGVAE 57  
 58 LSS--AMR-----NNSVPLRLDGRFVPHSCRYR-----LATIA-NESALG 96  
 58 LSGRCGWSPAEELNYTPGIGPAGFAFLGCRRYEDVMQNSALSCVDPLASLATNSHP 117  
 97 LEEGRVDLGLQEQESCLDGMESODVYISTVYTEVNLCEENMKKVPILTSLEFVAVLG 156  
 118 LGP-----CQDGWY--DTPGSSIVTEFNLVCAQSWKLDLQSCINAGFFRG 162  
 157 SPVSGOLSDRGRKNVLFATMAVOTGFSFLQIFSISEMFTVLFVIGMGLSNVYAFI 216  
 163 SLGVGYFADRFGRKICLIGTVLNNVSGVLMASPPYMSMLFRLGLGIVSKGNMAGYT 222  
 217 LGEIILG---KSVRIIFSTLGVCTFPANGVYMLPLFAFIRDMRLALATVPGVLYP 272  
 223 LITEFVGSGSRRTVATMYOMA-----FTVGLVALTGIAVALPFRWLOLAVSLPFLFL 277  
 273 LMFIFESPRLISORFREAEEDIIQAKAMNTAVPAVI-----FDSVEELNPLKQOK 326  
 278 YMCVPESPRWLSOKRNPFAIKIMHIAOKNKLPRADIKMLSEEDYTEKISP----- 332  
 327 AFLIDLFRTNIAIMTMSLLMLTSGVFALSLDAPNLHGDAYINCLFSLALIEIPAVI 386  
 333 -SFADLFRTPRLRKRFETIMYLMFTDSVLYQGLIHMGATSGNLYLDFYLSALVEIPGAF 391  
 387 TALLLRTLRRTIITIAVLEWGGVLLFLOLVVDVYFISIGVLMGKIGTSAFEMLY 446  
 392 IALITIDRGRIYPMASNLLAGAACLVFISP-DLHMNIIIMCGRMGITIAIMICL 450  
 447 FTAELPVTIRNNAVGTSPASRVGSIAPYFY-LGAVYRMLPYVMGSLVILGIFLT 505  
 451 VNAELPVTFRNLRAVWCSSLCIDIGITIPFYFRLEWQALPLILFAVLGLLAGVIL 510  
 506 FPESLGMFLPETLEOMQKVRKRSGRKTRDSMET 540  
 511 ILPETKGDALPETMKDAENL-----GRKAKPREMT 540

RESULT 7  
 US-08-647-397-2  
 ; Sequence 2, Application US/08647397  
 ; Patent No. 5972702  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Belier, David R.  
 ; APPLICANT: Brady, Kevin P.  
 ; TITLE OF INVENTION: OSTEOCLAST TRANSPORTER  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
 ; STREET: 600 Atlantic Avenue  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/647,397  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gates, Edward R.

REGISTRATION NUMBER: 31,616  
 REFERENCE/DOCKET NUMBER: B0801/7048  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-720-3500  
 TELEFAX: 617-720-2441  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 537 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-647-397-2

Query Match 22.1%; Score 630; DB 2; Length 537;  
 Best Local Similarity 30.0%; Pred. No. 3.2e-57;  
 Matches 165; Conservative 102; Mismatches 245; Indels 38; Gaps 12;

4 YDEVAFLGEMGFQF---LIFPLSASIIIPNGFNGSVFLAGTPEHRCRPDANLSAMR 63  
 3 FSEIILDRGSMGPFYLAHTLALPLILGANHNLQITATTPDHCHRPNNASL-EPW- 60  
 64 NNSVPLRLDGRFVPHSCRY--RLATIANFSAIGLEPGKVDLGLQEQESCLDGMES 120  
 61 --VLPLG-PNGK--PEKCLRFVHLPNASLPDYGATEP-----CIDGWLYN 102  
 121 QDVYISTVYTEVNLVCEENMKKVPILTSLEFVGVLLSGVSGOLSDRGRKNVLFATMAVQ 180  
 103 SF--KDTIVTEMDLVCGSKNKLKEMQSVFMAGILVGVGFELSDFRFRKRIILRWSYLL 160  
 181 TGFSEFLQIFSISEMFTVLFVIGMGLSNVYAFILGTEILGSVRIIFS-TLGVCTFF 239  
 161 AASGSSAAPPSELVAYMIFRFLCGCSISGISITLIINVEWVPTSTRAISSTTGYC--Y 218  
 240 ANGYMLPLFAFIRDMRLALATVPGVLYPLMFTPESPRLISORRREAEEDIIQOK 299  
 219 TIGQPLIPGLAAYVQWRWLOLSVSAFETISLSMWVPESTRMLVLSGKFSRLKTLQR 278  
 300 AAKM-----NTAVPAVIFDSVEELNPLKQOKAFIIDLFRTRNIAIMTMSLLMLT 352  
 279 VATPGRKKEGKRLVYEELKFMQKDITSAK-VKIGLSDLRVSLTRAVTCLSIAMPAT 337  
 353 SVGYALSLDAPNLHGDAYINCLFSLALIEIPAYITAMLLTLTPRTIITAAVLEWGGVYL 412  
 338 GRAVYSLAMGVEFGVNYIILQIFRGVDIPAKFTIILISYLRITOGFILLIAGVAI 397  
 413 LFIOLVVDVYFISIGVLMGKIGTSAFEMLYFTAELPVTIRNNAVGTSPASRVGS 472  
 398 IALIFVSSSEMQLRTALAVFGKGLSGSFSCLFITYSELVPLVLTQTMGSIINIAVRGS 457  
 473 IIAFYFVYLGAVYRMLPYVMGSLVILGIFLFPESLGMFLPETLEOMQKVRKRSRGK 532  
 458 MIAPLVKITGELQPIPIPNVITWMTLGLGSAFLELTLNRLPRTIIDIQ--DWYQOKX 515  
 533 KTRDSMETEE 542  
 516 KTKQEPKAEK 525

RESULT 8  
 US-09-572-147-2  
 ; Sequence 2, Application US/09572147  
 ; Patent No. 6420544  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lin Yue  
 ; APPLICANT: John Feld  
 ; APPLICANT: Harna Ellens  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE AND POLYPEPTIDE SEQUENCES  
 ; TITLE OF INVENTION: ENCODING MURINE ORGANIC ANION TRANSPORTER 5 (moatp5) AND  
 ; TITLE OF INVENTION: SCREENING METHODS THEREOF  
 ; FILE REFERENCE: GP-70622  
 ; CURRENT APPLICATION NUMBER: US/09/572,147  
 ; CURRENT FILING DATE: 2000-05-17  
 ; PRIOR APPLICATION NUMBER: 60/134,879

```

; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 545
; TYPE: PRF
; ORGANISM: MUS MUSCULUS
US-09-572-147-2

Query Match
  Best Local Similarity 21.3%; Score 606.5; DB 4; Length 545;
  Matches 161; Conservative 105; Mismatches 249; Indels 37; Gaps 12;

QY 4 YDEVIATLGEWGPORLLIFLLSASIIIPNGFNGSVVFLAGTEPHRCRVPDANLS----59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 FNDLKQGVGVGRFQOLIQTVMVYVAPRLMLASHMTLQNFATAIPRHCRPPANMLNSDGG 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 -SARNNSVPLRLDGEVPHSCRYLATIANFSALGLEPGRDVLGQLEQESCDGWE 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 LEAM-----LPDL-KQGR-PESCIRF-----PPHNGTEAN-----GTGVTEPCLDGMY 104
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 119 FSDQVYLVSTVTEWNLVCEDNMKVPLTTSLEFVGVLGSPVSGQLSDRGRKNVLEPATMA 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 105 YDNSTFSTVTEWNLVCSHRAPQLAQSLEFMGVLLGAMFGYLDRLGRKRVLLINT- 163
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 179 VGTGFS-FLQIFSIWEMFTVLVYVGMQISNYVVAFLIGTEILGKSVRIIFSTLGVCY 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 164 LQTVASGTCAAAYAPNTVYVYCFIRLLSGMSLAINCMTLNMEMPIHTRAYVGTG-LIG 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 238 FFAVGYMLLPLFAFIDRMMLLALTVPGLVPLMWFIPESPRLISGRPREADII 297
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 223 VYSIGQFLAGIAAVPHMRHLQLAVSVPFFVAFIYSWPFIESARWSSSGRLDYLRLAL 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 298 QKAKMNNATVPA-----VIFDSVEELNPLKQOKAFILDLFRTNIAITIMSLMLML 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 283 QVARIRINGKQEBGAKLSIEVLQTSLOKELTLNKGQASAMBLKCPRLRLFLCLSLMLMR 342
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 352 TSVGYFPLSDAPRLHGDAYLNCFLSALIEIPAYITAMILLRLPRRYIIAAVLEWGGV 411
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 343 TSPAYYGLVMDLGGFVSMYLIQVIGAVDLPKAFVCFIYNSMGRHPQOLASLLAGIC 402
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 412 LLEFQVLPVVDYFSLIGLVMGKFGITSAPSMYVFAELPYPLVNMVAGVYSTSRG 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 403 ILVNGIIPRHITIRSLAVLGCCLASNCIFLTGELYPRMIMOTGLMGSTMARVG 462
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 472 SIAPFVYVLYGAYNRLPYVMGSLVYLIGIFLFPESLGMTLPETLDQOKVWFRS- 530
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 463 SIYSPILISMATAEFPYSIFLFGAVPYAASAVTALLPETLGLPDTVDLKS----RSR 518
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 531 GKKTROSMETEE 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 519 GKQKQOOLEQOK 530
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-09-330-245A-2
; Sequence 2, Application US/09330245A
; Patent No. 6432631
; GENERAL INFORMATION:
; APPLICANT: GILEAD SCIENCES, INC. et al.
; TITLE OF INVENTION: NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER
; FILE REFERENCE: 240.1PCHW
; CURRENT APPLICATION NUMBER: US/09/330,245A
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/088,864
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/132,267
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 550
; TYPE: PRF

```

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; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: this information
; OTHER INFORMATION: is not available.
US-09-330-245A-2

Query Match
  Best Local Similarity 20.6%; Score 586; DB 4; Length 550;
  Matches 156; Conservative 104; Mismatches 256; Indels 40; Gaps 9;

QY 4 YDEVIATLGEWGPORLLIFLLSASIIIPNGFNGSVVFLAGTEPHRCRVPDANLSMR 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 FNDLKQGVGVGRFQOLIQTVMVYVAPRLMLASHMTLQNFATAIPRHCRPPADANLS--K 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 NNSVPLRL-RDGEVPHSCRYRL-----ATIANFSALGLEPGRDVLGQLEQESCD 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 NGCLEVYLPRLDQOGPESCLRTSPQWGLPPLNGTEAN-----GTGATPFC 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 LDGWFSDQVYLVSTVTEWNLVCEDNMKVPLTTSLEFVGVLGSPVSGQLSDRGRKNV 173
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 106 TDGWIYDNSTFSTVTEWNLVCSHRALROLAQSLEYVGVLLGAVVFGYLDRLGRKRV 165
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 FATMAVGTGFS-FLQIFSIWEMFTVLVYVGMQISNYVVAFLIGTEILGKSVRIIFST 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 166 ILNT-LQTVASGTCAAFAFPNFPYICAFRLSGMALAGISLNCMTLNVEMMPIHTRAYCY 224
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 LGVCFEFAVGYMLLPLFAFIDRMMLLALTVPGLVPLMWFIPESPRLISGRPRE 292
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 225 L-IGYVYSLGQFLAGVAVPHMRHLQLAVSVPFFVAFIYSWPFIESARWSSSGRLD 283
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 293 AEDIIQKAKMNNATVPA-----VIFDSVEELNPLKQOKAFILDLFRTNIAITIMSL 346
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 284 TLRALQVARIRINGKREBGAKLSMEVLRLSLQKELTMGQASAMBLKCPRLRLFLCLSL 343
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 LLMMLTSVGYFPLSDAPRLHGDAYLNCFLSALIEIPAYITAMILLRLPRRYIIAAVLE 406
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 344 MLMFATSPAYYGLVMDLGGFVSYLLIYIGAVDLPKAFVCFIYNSMGRHPQOMALL 403
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 407 WCGVGLLEFQVLPVVDYFSLIGLVMGKFGITSAPSMYVFAELPYPLVNMVAGVYST 466
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 404 LAGIICILNGVIRPDQOSIVRSLAVLGCCLASNCIFLTGELYPRMIMOTGLMGST 463
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 467 ASRVGSIIAPFVYVLYGAYNRLPYVMGSLVYLIGIFLFPESLGMTLPETLDQOKV 526
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 464 MARVGSIVSPILISMATAEFPYSIFLFGAVPYAASAVTALLPETLGLPDTVDLKS-- 521
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 527 WFRSGKKTROSMETEE 542
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 522 --RKGRQTRQOQEHOK 535
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-08-964-127-2
; Sequence 2, Application US/08964127
; Patent No. 6277565
; GENERAL INFORMATION:
; APPLICANT: Grandearl, Andrew David John
; TITLE OF INVENTION: NOVEL GENES ENCODING TRANSPORTER-LIKE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:

```





DB 265 NTRQPIITISIMQLSQSGINAVFYSTGI-----FKDAGVOEPYATIGA 311  
QY 388 -----AMLLRLTPRRYITIAAVLFMG-----GVLLFIQLVPDY----FLSIG- 428  
DB 312 GVNTIFTVSVFLVERAGRRL--HLIGGMAFCISILMTISLLKDNYSMSFCIGA 369  
QY 429 -LYMLGKFGITSAFSLVFTAEIYPTLVNNAVGTSTAS-----RVGSIAPFYVIG 482  
DB 370 ILVFAAFEEIGPG-PIPMFTVAELFGGPRPAMAAGCSNMTSNFLVGLLFPSSATFYL 428  
QY 483 AYNRMPLPYVMGSLTVLIGITFLF-FPESIGMTLPE 517  
DB 429 AY-----VFIVFTVFLVFWTFEFKVPETRGRTFEE 460

RESULT 14  
US-09-610-417-5  
Sequence 5, Application US/09610417  
Patent No. 6346374  
GENERAL INFORMATION:  
APPLICANT: Tartaglia, Louis A.  
Meng, Xun  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: PastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/610,417  
FILING DATE: 05-Jul-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/299,549  
FILING DATE: <UNKNOWN>  
ATTORNEY/AGENT INFORMATION:  
NAME: Melkielejohn, Ph.D., Anita L.  
REGISTRATION NUMBER: 35,283  
REFERENCE/DOCKET NUMBER: 07334/072002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 494 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-610-417-5

Query Match 8.2% Score 234.5; DB 4; Length 494;  
Best Local Similarity 25.2%; Fred. No. 6.7e-16;  
Matches 115; Conservative 76; Mismatches 156; Indels 109; Gaps 23;

QY 133 NLVGEDNKKVP-----LFTSLFVGVLLGSFVSQGLSDRFGKKN--VLEPAMAV 179  
DB 43 NYTLERSETPSSVLLTSLMSLSVAITSVGMIGSFSVGLFVNFRKMSMLIVNLAI 102  
QY 180 QTG--FSLQIFISJSMENFTLVFIYGM--GQISNYVAFTIGTEILLKSVRIITST--- 232  
DB 103 AGGCLMGFCCKI-ABSEVEMLIIGRLIIGFCIGTGFVPMYI--GEISPTALRGAFGLTNO 159  
QY 233 LGVCFPAVGVMLLPLFAFYI-----RQMRMLIALIV-PSVLCVPLMWFIPESPRWLISO 287

DB 160 LGI-----VIGILVQIIGLAKVILCTEDLWPLLGLFTLLPAILQCAALPFCPESPRELLIN 215  
QY 288 RFRFE-----AEDIIQKAKANNNAVPAVIDSVBELNPLKQKQAFIIDLFRFR 336  
DB 216 RKEEKAKKEIQLRLMGTEDEVAQDIOEMKD-----ESMMSQEKQVLELFRAP 264  
QY 337 N-----IAIWTISLLMTSVGYFALSIDAPNLHGDAYINCFALSLEIYATIT--- 387  
DB 265 NTRQPIITISIMQLSQSGINAVFYSTGI-----FKDAGVOEPYATIGA 311  
QY 388 -----AMLLRLTPRRYITIAAVLFMG-----GVLLFIQLVPDY----FLSIG- 428  
DB 312 GVNTIFTVSVFLVERAGRRL--HLIGGMAFCISILMTISLLKDNYSMSFCIGA 369  
QY 429 -LYMLGKFGITSAFSLVFTAEIYPTLVNNAVGTSTAS-----RVGSIAPFYVIG 482  
DB 370 ILVFAAFEEIGPG-PIPMFTVAELFGGPRPAMAAGCSNMTSNFLVGLLFPSSATFYL 428  
QY 483 AYNRMPLPYVMGSLTVLIGITFLF-FPESIGMTLPE 517  
DB 429 AY-----VFIVFTVFLVFWTFEFKVPETRGRTFEE 460

RESULT 15  
US-08-355-844-3  
Sequence 3, Application US/08355844  
Patent No. 5940307  
GENERAL INFORMATION:  
APPLICANT: Fischbarg, Jorge  
Applicant: Czegledy, Ferenc  
Applicant: Iserovich, Pavel  
Applicant: Li, Jun  
Applicant: Cheung, Min  
TITLE OF INVENTION: A METHOD FOR PREDICTING PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESS: Brumbaugh, Graves, Donohue & Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/355,844  
FILING DATE: 14-DEC-1994  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Tang, Henry Y.S.  
REGISTRATION NUMBER: 29,705  
REFERENCE/DOCKET NUMBER: A29927-50/29910  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-408-2586  
TELEFAX: 212-765-2519  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 492 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Human  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..492  
OTHER INFORMATION: Facilitative glucose transporter

OTHER INFORMATION: Glut1 protein  
US-08-355-844-3

Query Match 7.8%; Score 222; DB 2; Length 492;

Best Local Similarity 24.0%; Pred. No. 1.3e-14;  
Matches 117; Conservative 74; Mismatches 175; Indels 122; Gaps 21;

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QY      119 FSDPVLSFYVTENLVCEEDNMKPIPLTSLFEVGLLGSFVSGQLSDRFRGK-----NV 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      52 YGESILPTLTLTMS-----LSVAIFSVGMIGSFVSGLFVNRFRGRSMIMMNL 101
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      173 LFAFMANVQGESFLQFSTISWEN-----FTVLFEVYVGMGOISNIVYVAFLTGT 219
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      102 LAFVSAYVLMGFSKL--GKSEMLILGRFLIGYCGLTIGFVPMYVGEVSPTRAFGALGT 158
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      220 ELGKSVRIIEFTLGYCTEPFVAGVMLPLFAVPI---RD-WRMILLALVPGVLCVPLM 274
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      159 -----LHQLGI---VVGILIAQVGLDSIMGNDIMPLLSIIIFIPALLQCIYI 204
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      275 WFIPESPRMILISQRRREAEITQAKAKNNNTAVPAVIFDSVEELNPLKQ-----K 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      205 PCPESEPRFLINRNEENRAKSVLK--KLNGTA-----DYTHDLOEMKEESROMREKK 256
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      327 AFITLDEPRTNR-----IAIMTISLLMMLTSGYFALSIDAPNLHGDAYLNCFTSALI 380
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      257 VTILELFRSPAYROPILIAVYLOLSQOLSGINAVFYSTSI-----FEKAGY 303
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      381 EIPAYIT-----AMLLRLTPRR--YIIAAYLFWGGVILFLOLVPDY-- 423
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      304 QQEYVATIGSGIVNTAFVYSLFVERAGRRLHLIGLAGMAGQAILMTIALALLQLPW 363
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      424 --FLISGLVLMGKIGITSAFS-----MLVYFTELPTLVNNAVGVTASRVGS-IIA 475
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      364 MSTLSIVAI--FGVYAFEEVGPGLPWFIVAELESQGRPAIAVAGSMTSNFTIVG 419
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      476 PYEVYLGAVYRMPLIYVMSLTVLIGIFTLF--PPESLGMTLPETLEOMQVKWFRSGKKT 534
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      420 MCFQYVQQLCGPYVFIIFVLLVLFIRYFYKVPETKGRTEDEI-----ASGFRQGGAS 473
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      535 RDSMETEE 542
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      474 QSDKTPPE 481
```

Search completed: July 3, 2003, 12:39:03  
Job time : 21 secs